

## SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: ~~11-04-02~~  
 Searcher: Beverly 24994  
 Terminal time: 20  
 Elapsed time: \_\_\_\_\_  
 CPU time: \_\_\_\_\_  
 Total time: 25  
 Number of Searches: \_\_\_\_\_  
 Number of Databases: 1

## Search Site

\_\_\_\_\_ STIC  
 \_\_\_\_\_ CM-1  
 \_\_\_\_\_ Pre-S

## Type of Search

\_\_\_\_\_ N.A. Sequence  
 \_\_\_\_\_ A.A. Sequence  
 \_\_\_\_\_ Structure  
 \_\_\_\_\_ Bibliographic

## Vendors

\_\_\_\_\_ IG Suite  
 \_\_\_\_\_ STN  
 \_\_\_\_\_ Dialog  
 \_\_\_\_\_ APS  
 \_\_\_\_\_ Geninfo  
 \_\_\_\_\_ SDC  
 \_\_\_\_\_ DARC/Questel  
☒ Other CGN





FEATURES		Location/Qualifiers		RESULT 2	
SOURCE					
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CDS		41.. 970		AF04285.1 GI:2832259	
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		/locus_tag="Zm_011.35"		adenosine-5'-phosphosulfate-kinase (EC 2.7.1.25) from Catharanthus	
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		/locus_tag="Zm_011.35"		Arabidopsis (Accession No. AF04285) and an isoform (akr2) from	
		/locus_tag="Zm_011.35"		Schiffmann, S. and Schwen, J.D.	
		/locus_tag="Zm_011.35"		Submitted (23-JAN-1998) Biochemie der Pflanzen, Ruhr-Universität	
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Db	452	ATGATACAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATG	511	144..860	/note="phosphatase 5'-adenylyl sulfate on 3'-hydroxyl group"	
Qy	568	GTTCATGTCAGAGCAGCAGCTACATGATGATGATGATGATGATGATGATGATG	627		/note="similar to yeast Aps kinase (MER14); SwissProt: P18466; Aps kinase (yeast). SwissProt Accession Number P18466;	
Db	512	CTTATCAAGCAAGGAAAGAACTACTATCTTATGATGATGATGATGATGATGATG	571		adenosine 5'-phosphoribosyl transferase (EC 2.7.1.11) Aps kinase (yeast). SwissProt Accession Number P18466;	
Qy	628	AAATGATGATTAAGCTTATGATGATGATGATGATGATGATGATGATGATGATG	687		/evidence=experimental	
Qy	572	GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	631		/product="Aps kinase"	
Qy	688	ATGCAAGCAAGCTTCTTATGATGATGATGATGATGATGATGATGATGATGATG	747		/translat="MIAGASLGLIOMASPGLEFDSKSNKSNVWVWVACYSKDS	
Qy	632	ATGCAAGCAAGCTTCTTATGATGATGATGATGATGATGATGATGATGATGATG	691		TRYSKSNKSNVWVWVACYSKDS	
Db	748	CAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	807		TRYSKSNKSNVWVWVACYSKDS	
Qy	812	ATGCAAGCAAGCTTCTTATGATGATGATGATGATGATGATGATGATGATGATG	871		TRYSKSNKSNVWVWVACYSKDS	
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TRANSIT	3					
LOCUS	AT005238					
DEFINITION	Arabidopsis thaliana Aps kinase mRNA, complete cds.					
VERSION	005238.1					
KEYWORDS	1 G1:450234					
ORGANISM	Arabidopsis thaliana					
REFERENCE	1 (bases 1 to 1077)					
AUTHORS	Lee-S. and Leustek.T.					
TITLE	Arabidopsis thaliana Aps kinase, core eukaryotic					
REFERENCE	2 (bases 1 to 1077)					
AUTHORS	Lee-S. and Leustek.T.					
TITLE	Arabidopsis thaliana Aps kinase, core eukaryotic					
REFERENCE	3 (bases 1 to 1077)					
AUTHORS	Lee-S. and Leustek.T.					
TITLE	Arabidopsis thaliana Aps kinase, core eukaryotic					
FEATURES						
SOURCE						

Qy	411	TGTCAGCATGGGAATGACATATATTTATGTCACATGCTGATGTCACATGCTG	470	24.48; Score 296.4; DB 8; Length 1077;	
Db	367	TGTCAGCATGGGAATGACATATATTTATGTCACATGCTGATGTCACATGCTG	426	Heat Local Similarity 68.0%; Pred. No. 6.5e-50;	
Qy	531	CAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	590	Melchies 4.00; Consensitive 0; Hammetts 196; Indels 6; Gaps 1;	
Db	367	CAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	426	BASE COUNT 300 a 178 c 256 g 343 t	
Qy	591	CGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	650	ORIGIN	
Db	427	GTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	486	Query Match	
Qy	651	CAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	710	Heat Local Similarity 68.0%; Pred. No. 6.5e-50;	
Db	487	CAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	546	Melchies 4.00; Consensitive 0; Hammetts 196; Indels 6; Gaps 1;	
Qy	711	CGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	770	BASE COUNT 300 a 178 c 256 g 343 t	
Db	547	CGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	606	ORIGIN	
Qy	771	CGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	830	Query Match	
Db	607	GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	666	Heat Local Similarity 68.0%; Pred. No. 6.5e-50;	
Qy	831	CGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	890	Melchies 4.00; Consensitive 0; Hammetts 196; Indels 6; Gaps 1;	
Db	667	GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	726	BASE COUNT 300 a 178 c 256 g 343 t	
Qy	891	CGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	950	ORIGIN	
Db	727	TACGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	780	Query Match	
Qy	951	GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1010	Heat Local Similarity 68.0%; Pred. No. 6.5e-50;	
Db	781	GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	840	Melchies 4.00; Consensitive 0; Hammetts 196; Indels 6; Gaps 1;	



[illegible][illegible]































GenCore version 5.1.3  
Copyright: (c) 1995 - 2002 CompuLink Ltd.

ON nucleic - nucleic search, using sw model

Run on: November 1, 2002, 22:55:32 : Search Time 234 Seconds

11/15: 62427-423 NA1180 cell updates/sec

US-09-720-384a-3

Sequence: 1 ggcgttccttcattcatca.....aaataaaataaaataaa 1217

Scoring table: TSPWRTK.WGC

Gap 10.0 - Gapext 1.0

Searched: 1736435 seps, 83845721 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 10%

Listing first 45 summaries

Database : N\_Geneseq.0328021\*

- 1: /SIDSI/sgcdgata/geneseq/geneseq-emb/NA1980.DAT\*
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- 3: /SIDSI/sgcdgata/geneseq/geneseq-emb/NA1982.DAT\*
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- 21: /SIDSI/sgcdgata/geneseq/geneseq-emb/NA2000.DAT\*
- 22: /SIDSI/sgcdgata/geneseq/geneseq-emb/NA2001.DAT\*
- 23: /SIDSI/sgcdgata/geneseq/geneseq-emb/NA2002.DAT\*
- 24: /SIDSI/sgcdgata/geneseq/geneseq-emb/NA2003.DAT\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1217	100.5	1217	NA250165	NA250165
2	359.6	29.5	938	NA250165	Wheat Adenylsulphate kinase
3	338.8	27.8	936	NA250162	Soybean Adenylsulphate kinase
5	316.2	26.0	890	NA250159	Arabidopsis thaliana
6	296.4	24.4	1068	NA235266	Arabidopsis thaliana
8	296.4	24.4	1175	NA235268	Arabidopsis thaliana
9	290	23.8	1130	NA24070	Arabidopsis thaliana

10	288.4	23.7	1133	21	AMC36627	Arabidopsis thaliana
11	263.6	21.7	917	21	AAZ08337	A. thaliana gene 1
12	263.6	21.7	917	21	AAZ08337	Arabidopsis thaliana
13	2225	18.5	718	21	AAZ01190	Arabidopsis thaliana
14	198.2	16.3	483	21	AAZ01135	Arabidopsis thaliana
15	198.2	16.3	483	21	AAZ01135	Arabidopsis thaliana
16	198.2	16.3	483	21	AAZ01135	Arabidopsis thaliana
17	152.8	13.4	521	21	AAZ01064	Knight adenylsulphate kinase
18	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
19	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
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22	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
23	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
24	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
25	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
26	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
27	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
28	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
29	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
30	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
31	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
32	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
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35	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
36	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
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39	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
40	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
41	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
42	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
43	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
44	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae
45	136.4	12.9	1136	21	AAZ08557	Saccharomyces cerevisiae

## ALIGNMENTS

RESULTS 1  
ID AM250160 standard; cDNA; 1217 BP.

AM250160

04-MAY-2000 (first entry)

Corn Adenylsulphate kinase-2 cDNA clone.

AD Adenylsulphate kinase; Adenosine-5'-phosphogluconate kinase; APS kinase;  
3'-Phospho-adenosine-5-phosphosulphate; PAPS; sulphate assimilation;  
KW corn; cDNA p016.ctc40rb; transgenic plant; screen; antibody ss.

OS Zea mays.

XX Key

XX Location/Qualifiers

XX /tag- a

XX /product- "Corn APS kinase-2"

XX /note- "Derived from clone p016.ctc40rb"

XX MO200004165-A1.

XX 27-JAN-2000.

XX 13-JUL-1999; 99MO-US15809.

XX 14-JUL-1998; 98US-0092833.

XX (GUPP) DU POINT DE NEKROUS a co E. I.









[illegible]











[illegible]























QY 470 GATACGAGAAATCTGCGACAAAGAGCTGTGTGTGTATGATACAGAGCATGTGT 529  
 DB 61 GAAAGCGAGAGTCTTAATCAGAGGTGTGTGTGTGTATGATACAGAGCTGTGTG 120  
 QY 530 TCGGAGAAAGGT 569  
 DB 121 TCGGAGAAAGGT 180  
 QY 590 ACTGATGTACTGT 649  
 DB 122 TCGGAGAAAGGT 180  
 QY 590 ACTGATGTACTGT 649  
 DB 181 TGAATATCTGT 240  
 QY 650 GCGAGAGCGTGAAGAAATATATATATATATATATATATATATATATATATAT 709  
 DB 241 GCGAGAGCGTGAAGAAATATATATATATATATATATATATATATATATATATAT 300  
 QY 710 GCTGT 769  
 DB 301 GCTGT 360  
 QY 770 GCTGT 802  
 DB 361 GCTGT 420  
 QY 803 GCTGT 862  
 DB 421 GTTTCATGATCATCTCTCTCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480  
 QY 863 CTT 865  
 DB 481 CTT 483

## RESULT 15

ARC50161:  
 AC ARC50161 standard; cDNA: 431 BP.  
 AT ARC50161:  
 DT 04-MAY-2000 (first entry)  
 XX  
 XX Rice Adenylylsulphate Kinase cDNA clone.  
 XX  
 KW Adenylylsulphate Kinase: Adenosine-5-phosphosulphate Kinase; APS kinase;  
 KW 3'-phospho-adenosine-5'-phosphosulphate: PAPS; sulphate assimilation;  
 XX Rice; clone rl0n:pk112.011; Transgenic plant; screen; antibody; 48.  
 XX  
 OS Oryza sativa.  
 XX

Key Location/Qualifiers  
 FT mat\_peptide 55..408  
 FT name 1  
 FT /product: "Rice APS Kinase"  
 FT /note: "Derived from clone rl0n:pk112.011"

WC020004165-A1.  
 XX  
 PD 27-JAN-2000.  
 XX  
 PD 13-JUL-1999; 99MC-0851509.  
 XX  
 PD 14-JUL-1998; 98US-0092333.  
 XX  
 PA (DIPO) DU PONT DE NEMOURS & CO S. I.  
 XX  
 XX Falco SC, Allen SK, Anderson SL.  
 XX  
 XX WPI: 2000-182430/16.  
 DR P-FSDB: AX44750.  
 XX  
 XX New nucleic acid molecule and chimeric gene encoding an adenosine-5'-  
 XX phosphosulphate kinase, useful for altering expression of sulfate  
 XX assimilation protein in plants .

XX Claim 3, Page 32; 42pp; English.

XX The present sequence is a cDNA encoding rice adenylylsulphate kinase  
 XX obtained from clone rl0n:pk112.011 derived from rice 15 day leaf; rl0n  
 XX cDNA library. APS kinase is a sulphate assimilation protein, that  
 XX catalyses the conversion of adenosine-5'-phosphosulphate (APS) to  
 XX adenosine-5'-phosphosulphate (PAPS). PAPS is used as  
 XX probes and primers to identify, obtain and synthesise sulphate  
 XX assimilation proteins from other plants. It is also used to produce  
 XX antibodies that are used to screen and isolate cDNA clones of  
 XX producing antibodies that are used to screen and isolate cDNA clones.

XX Sequence 431 BP; 126 A; 78 C; 112 G; 112 T; 3 other:

Query Match 10 24; Score 197.2; Dn 21; Length 431;  
 Matches 253; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 424 GAAATGCTAT 483  
 DB 66 GAGGCGTCCATATCTTGTGGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 125  
 QY 484 CTGGCGCAAAAGGCTGT 543  
 DB 126 ACTGAGCAAGAAAGGCTGT 185  
 QY 544 TCTGTATGT 603  
 DB 186 CTGGCATGT 245  
 QY 604 TGT 663  
 DB 246 TGT 305  
 QY 664 GAAAT 723  
 DB 306 TGAAT 365  
 QY 724 ATGT 770  
 DB 366 ATTCGCAAGTTCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 412

Search completed: November 1, 2002, 23:43:31  
 Job time : 239 secs



Genome version 5.1.3  
 Copyright (c) 1991-2002 Comugen Ltd.  
 OM nucleic - nucleic search, using sw model  
 Run on: November 1, 2002, 21:39:32, Search time 53 seconds  
 540.301 Million cell updates/sec  
 Title: US-09-720-384a-3  
 Nucleic score: 1217  
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 Scoring table: IDENTITY NYC  
 Gapop 10.0, Gapext 1.0

Searched: 39353 seqs, 122810752 residues  
 Total number of hits satisfying chosen parameters: 767066  
 Minimum DB seq length: 0  
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 Maximum Match 1004  
 Listing first 45 summaries  
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 2: /cgn2\_6/prodata/2/ins/3A.COMB.seq.\*  
 3: /cgn2\_6/prodata/2/ins/3A.COMB.seq.\*  
 4: /cgn2\_6/prodata/2/ins/3A.COMB.seq.\*  
 5: /cgn2\_6/prodata/2/ins/3A.COMB.seq.\*  
 6: /cgn2\_6/prodata/2/ins/3A.COMB.seq.\*  
 Pred. No. is the number of results predicted by chance to have a  
 number of results as high as the one actually obtained. The  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	Match	Length	ID	Description
1	156.4	12.9	1160	US-09-153-310-41	Sequence 41, Appl
2	199	11.4	2006	US-08-379-561-4	Sequence 4, Appl
3	45.6	3.7	1323	US-09-413-422-3	Sequence 3, Appl
4	45.6	3.7	1323	US-09-413-422-3	Sequence 3, Appl
5	45.6	3.7	1323	US-09-413-422-3	Sequence 3, Appl
6	45.6	3.7	1323	US-09-413-422-3	Sequence 3, Appl
7	43.4	3.6	2447	US-09-011-969-14	Sequence 14, Appl
8	42.8	3.5	12001	US-08-458-5684-11	Sequence 11, Appl
9	42.4	3.5	320	US-09-165-264-7	Sequence 7, Appl
10	42.4	3.5	320	US-09-165-264-7	Sequence 7, Appl
11	42.4	3.5	1481	US-08-474-3796-87	Sequence 87, Appl
12	42.4	3.5	3131	US-07-684-3526-21	Sequence 21, Appl
13	42.4	3.5	3131	US-07-684-3526-21	Sequence 21, Appl
14	42.4	3.5	3131	US-08-206-1889-21	Sequence 21, Appl
15	42.4	3.5	3131	US-08-206-1889-21	Sequence 21, Appl
16	42.4	3.5	3131	US-08-206-1889-21	Sequence 21, Appl
17	41.4	3.4	320	US-09-165-264-7	Sequence 7, Appl
18	41.4	3.4	7218	US-08-232-463-14	Sequence 14, Appl
19	41.4	3.4	30001	US-08-125-969-1	Sequence 1, Appl
20	41.4	3.4	30001	US-08-125-969-1	Sequence 1, Appl
21	40.8	3.4	320	US-09-165-264-13	Sequence 13, Appl
22	40.6	3.3	1340	US-08-377-001-2	Sequence 2, Appl
23	40.6	3.3	1340	US-08-377-001-2	Sequence 2, Appl
24	40.4	3.3	15231	US-09-126-1516-6	Sequence 6, Appl
25	40.2	3.3	1420	US-08-305-9655-3	Sequence 3, Appl
26	40.2	3.3	1420	US-08-305-9655-3	Sequence 3, Appl
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44	39.8	3.2	258	US-08-596-844-13	Sequence 13, Appl
45	39.8	3.2	258	US-08-596-844-13	Sequence 13, Appl

## ALIGNMENTS

US-09-153-310-41  
 US-09-153-310-41 Application US/09153310  
 Patent No. 6,326,184  
 GENERAL INFORMATION:  
 APPLICANT: Christian, Claes  
 Hansen, Jorgen  
 Johannesen, Ela Francke  
 Johannesen, Peter Kall  
 Sorensen, Brian Boel  
 TITLE OF INVENTION: Method of producing a composite  
 fermented beverage using genetically modified yeast

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS: Lardner

STREET 3000 K Street, N.W.

CITY: Washington

STATE: DISTRICT OF COLUMBIA

COUNTRY: USA

ZIP: 20007-5109

COMPUTED BY: IBM PC

OPERATING SYSTEM: DOS

COMPUTER: IBM Compatible

CURRENT APPLICATION DATA: Windows Version 2.0

APPLICATION NUMBER: US/09153310

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA: <unknown>

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Bert, Stephen A, 768

REFERENCE/DOCKET NUMBER: <unknown>

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-672-5393

TELEX: <unknown>

SEQUENCE CHARACTERISTICS:

LENGTH: 1160 base pairs

TYPE: nucleic acid

TOPOLOGY: Linear

MOLECULE TYPE: Genomic DNA

DESCRIPTION: SEQ ID NO: 41

US-09-153-310-41

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Query Match      12.9% Score 156.4; DB 4; Length 1160;
Best Local Similarity 60.4%; Freq. No. 4.6e-31;
Matches 278; Conservative 0; Mismatches 176; Indels 6; Gaps 1;

Oy 470 GATGACAGAAATTCGTGGCAAAAGCTCTGCTGTGATGACAGAGCTCAGTGT 529
Db 420 GACTATAGAAATTAAGAGCGAGGAGGCTGCTGTGATGACAGAGCTCAGTGT 479
Oy 530 TCGGAAAGATTCCTTCACAGCTGAGTGTGATGATGATGATGATGATGATG 589
Db 430 TCGGAAAGATTCCTTCACAGCTGAGTGTGATGATGATGATGATGATGATG 489
Oy 590 AGGTATATATATATATATATATATATATATATATATATATATATATAT 649
Db 540 GTATATATATATATATATATATATATATATATATATATATATATATAT 599
Oy 650 GCGAAGACCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 709
Db 600 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 659
Oy 710 GCTGTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 769
Db 660 GCTGTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719
Oy 770 CTGCTGCTACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 823
Db 720 CTGCTGCTACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 779
Oy 824 AATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883
Db 780 GATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 839
Oy 884 AAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 923
Db 840 AAGAGGTCATGATGATGATGATGATGATGATGATGATGATGATGATG 879

RESULT 2
US-08-232-463-14/G
Sequence 4, Application US/08879561
Patent No. 5817482
GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
COMPLETION DATE: 08/07/96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
ATTORNEY: Incyte Center Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq for Windows Version 2.0
APPLICATION NUMBER: US/08879561
FILING DATE: Retrosult
PRIORITY DATE: 08/07/96
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: INFORMATION:
REGISTRATION NUMBER: 36,749
ATTORNEY: Billings, Lucy J.
REFERENCE/ACCT NUMBER: FF-0325 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2506 base pairs
STRANDEDNESS: single
TOPOLOG: linear
FEATURES:
LIBRARY: LUNG0702
CLONE: 373887
US-08-879-561-4
Query Match      11.4% Score 139; DB 1; Length 2506;
Best Local Similarity 26.26%; Freq. No. 2.4e-06;
Matches 24; Conservative 0; Mismatches 185; Indels 6; Gaps 1;

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Db 249 TCGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 308
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Db 309 GCTCATAGCTCTCAATAAATTAATTTTATCTGCTGTGATGATGATGATG 368
Oy 677 AGAGTGTGCTGAGTGGCAAGCTTTTCTGATGCTGTGATGATGATGATG 736
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Oy 791 ACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 850
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Oy 851 GCTCTTTCACAGCTGCTAGTACAGAGAGATTAAGGTTTCTGATGATGAT 910
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Db 609 TGTGAAAGGACAGAGCCCTCGATGCTGTGATGATGATG 645

RESULT 3
US-08-232-463-14/G
Sequence 14, Application US/0832463
Patent No. 5817482
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHUEFLINGER, F.
APPLICANT: SCHUEFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
COMPLETION DATE: 08/07/96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
ATTORNEY: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0590
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
REFERENCE/ACCT NUMBER: PC-050/AS-DOS

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1 SOFTWARE: Patent Release 41.0, Version 41.25  
 2 CURRENT RELEASE DATE: 08/09/93164  
 3 APPLICATION NUMBER: US/09/232.463  
 4 FILING DATE: 1998-05-18  
 5 CLASSIFICATION: 435  
 6 PUBLICATION NUMBER: US/07/935.313  
 7 APPLICATION NUMBER: 08/93164  
 8 FILING DATE: 1998-05-18  
 9 FILING DATE: 1998-05-18  
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 99 FILING DATE: 1998-05-18  
 100 FILING DATE: 1998-05-18

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 QY 361 ACAGCGCGCGGGAGCGCCGACGACCCGATGAGGAGACCTGTATCTGACAT 420  
 DB 1408 RRRER 1349  
 QY 421 TGGAGATCACTATTTATGCGACATCTCTGATGACATCTGATGACAGAA 480  
 DB 1348 RRRER 1289  
 QY 481 ATGTGCGGACAAAGCGCTGTGTATGATGACGACGATCACTGTCTGCGAAG 540  
 DB 1288 RRRER 1229  
 QY 541 TACTCTGCGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 DB 1228 RRRER 1169  
 QY 601 TGTGTCGACATCTGACATGCGCTAAATGAGATTTAAGCTTTAGCGAGACG 660  
 DB 1168 RRRER 1109  
 QY 661 TCGCAAAATACAGAGTGTGCGATGCGCAAG 697  
 DB 1108 RRRER 1072

RESULT 4  
 US-09-413-452-3  
 1 Sequence 3, Application US/09/13452  
 2 Patent No. 6083540  
 3 APPLICANT: Thorsen, T.  
 4 APPLICANT: Thorsen, H.  
 5 APPLICANT: Thorsen, H.  
 6 APPLICANT: Thorsen, H.  
 7 TITLE OF INVENTION: PROCESS FOR STABILIZING PROTEINS IN AN  
 8 FILE REFERENCE: DPG014.001APC

1 SOFTWARE: Patent Release 41.0, Version 41.25  
 2 CURRENT RELEASE DATE: 08/09/93164  
 3 APPLICATION NUMBER: US/09/232.463  
 4 FILING DATE: 1998-05-18  
 5 CLASSIFICATION: 435  
 6 PUBLICATION NUMBER: US/07/935.313  
 7 APPLICATION NUMBER: 08/93164  
 8 FILING DATE: 1998-05-18  
 9 FILING DATE: 1998-05-18  
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 99 FILING DATE: 1998-05-18  
 100 FILING DATE: 1998-05-18

Query Match 3.7%, Score 45.6, DB 3: Length 1323;  
 Best Local Similarity 52.7%; Pred. No. 0.017;  
 Matches 99; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
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 DB 1126 TAT 1185  
 QY 1090 ATAAGATCTGTGTGTGTCACATGATGATGATGATGATGATGATGATGAT 1149  
 DB 1186 TTGAGGCTCTTATCTGCGTGGTCTGATTTCCAACTATCTATGATGATGAT 1245  
 US-09-413-452-3  
 1 Sequence 3, Application US/09/13068  
 2 Patent No. 6083540  
 3 APPLICANT: Thorsen, T.  
 4 APPLICANT: Thorsen, H.  
 5 APPLICANT: Thorsen, H.  
 6 APPLICANT: Thorsen, H.  
 7 TITLE OF INVENTION: ACIDIC ENVIRONMENT WITH A HIGH-ESTER PECTIN  
 8 FILE REFERENCE: DPG014.001APC  
 9 CURRENT APPLICATION NUMBER: 08/93164  
 10 EARLIER FILING DATE: 1998-05-18  
 11 EARLIER FILING DATE: 1998-05-18  
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 14 EARLIER FILING DATE: 1998-05-18  
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1 MOLECULE TYPE: CDNA
2 FEATURE
3 NAME/KEY: CDS
4 LOCATION: 743..1951
5 FEATURE
6 NAME/KEY: misc_feature
7 LOCATION: 1852
8 OTHER INFORMATION: /note="1, shift in reading frame
9 OTHER INFORMATION: may occur at this residue."
10 PCT-US91-02714-20

Query Match          3.58; Score 42.4; DB 5; Length 3131;
Best Local Similarity 64.04; Pred. No. 0.16;
Matches 64; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1118 AAANGCATCACTAGTAGAAGTACAGAGGTACGTTCTATTCAGAACGATATGGA 1177
DB 2871 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1178 TTATCTGTTTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1217
DB 2811 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2811 TTCTGTTGTAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2772

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Search completed: November 2, 2002, 01:42:23  
 Job time : 73 secs

GenCode version 5.1.3  
Copyright (c) 1993 - 2002 Camgen Ltd.

OW nucleic - nucleic search, using sw model

Run on: November 1, 2002, 23:00:32, search time 1725 seconds  
522.200 Million call updates/sec

Title: US-09-720-384a-3

Perfect score: 1217

Sequence: 1 ggcgttcctttctctca.....aaataaaataaaataaa 1217

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapex: 1.0

Searched: 1735207 seep, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST\*

1: en:etha:.\*  
2: en:etha:.\*  
3: en:etha:.\*  
4: en:etha:.\*  
5: en:etha:.\*  
6: en:etha:.\*  
7: en:etha:.\*  
8: en:etha:.\*  
9: en:etha:.\*  
10: en:etha:.\*  
11: en:etha:.\*  
12: en:etha:.\*  
13: en:etha:.\*  
14: en:etha:.\*  
15: en:etha:.\*  
16: en:etha:.\*

Pred. No. is the number of results predicted by chance to have a  
maximum DB seq length of 200000000 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	48.5	675	10 BE37876	BE37876 DQ1_22.A0
2	583.4	47.9	691	10 BE35111	BE35111 DQ1_111.B
3	496.2	31.6	726	9 AW92943	AW92943 DQ1_120
4	496.2	31.6	726	9 AW92946	AW92946 DQ1_120
5	400.2	32.9	699	10 BE361874	BE361874 DQ1_62.G0
6	344.8	28.3	421	10 BE494142	BE494142 DQ1_175.G0
7	344.8	28.3	421	10 BE494142	BE494142 DQ1_175.G0
8	318.8	26.2	591	10 BE373562	BE373562 DQ1_175.G0
9	318.8	26.2	591	10 BE373562	BE373562 DQ1_175.G0
10	304.4	25.0	536	9 AW50397	AW50397 EST131445
11	294.2	23.4	714	10 BM407095	BM407095 EST131445
12	284.2	22.7	772	10 BE313666	BE313666 DQ1_120
13	275.2	22.6	748	10 BE313666	BE313666 DQ1_120
14	265.6	21.8	727	9 AW50397	AW50397 EST131445
15	265.6	21.8	727	9 AW50397	AW50397 EST131445
16	265.6	21.8	727	9 AW50397	AW50397 EST131445
17	261.6	21.5	786	10 BE178754	BE178754 EST159595

18	259.6	21.3	596	9 AW509923	AW509923 DQ1_120
19	259.6	21.3	596	9 AW509923	AW509923 DQ1_120
20	259.6	21.3	596	9 AW509923	AW509923 DQ1_120
21	218.2	17.9	722	10 BE409898	BE409898 DQ1_57.D0
22	215.8	17.9	722	10 BE409898	BE409898 DQ1_57.D0
23	215.8	17.9	722	10 BE409898	BE409898 DQ1_57.D0
24	208.4	17.1	631	9 AW73147	AW73147 AW52270
25	205.6	16.9	516	9 AW247472	AW247472 AW52270
26	205.6	16.9	516	9 AW247472	AW247472 AW52270
27	193.6	15.9	609	9 AW30778	AW30778 DQ1_120
28	171.6	14.1	809	9 BE19100	BE19100 DQ1_120
29	159.6	13.1	839	9 AW691426	AW691426 DQ1_120
30	159.6	13.1	839	9 AW691426	AW691426 DQ1_120
31	137.2	12.9	681	10 BE72846	BE72846 DQ1_120
32	137.2	12.9	681	10 BE72846	BE72846 DQ1_120
33	137.2	12.9	681	10 BE72846	BE72846 DQ1_120
34	135.2	12.8	1053	12 CN5060P	CN5060P DQ1_120
35	135.2	12.8	1053	12 CN5060P	CN5060P DQ1_120
36	135.2	12.8	1053	12 CN5060P	CN5060P DQ1_120
37	135.2	12.5	741	12 AQ365502	AQ365502 DQ1_120
38	135.2	12.5	741	12 AQ365502	AQ365502 DQ1_120
39	135.2	12.5	741	12 AQ365502	AQ365502 DQ1_120
40	135.2	12.5	741	12 AQ365502	AQ365502 DQ1_120
41	135.2	12.5	741	12 AQ365502	AQ365502 DQ1_120
42	135.2	12.5	741	12 AQ365502	AQ365502 DQ1_120
43	135.2	12.5	741	12 AQ365502	AQ365502 DQ1_120
44	135.2	12.5	741	12 AQ365502	AQ365502 DQ1_120
45	135.2	12.5	741	12 AQ365502	AQ365502 DQ1_120

## ALIGNMENTS

RESULT 1  
BE37876 DQ1\_22.A06\_g1.A002 Dark Grown 1 (DQ1) Sorghum bicolor CDMA, mRNA  
sequence.  
BE37876 1 GI:9299433  
EST  
Sorghum bicolor  
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Chlorophyta; Agrostophyta; Liliopsida; Poaceae; Poaceae; PAC  
Chromatids; Antepodeal; Mesophyll; Scabrous; PAC  
1 (bases 1 to 675)  
Cordonnier-Fratt M.-M., Gingle A., Suleman M. and Pratt  
An EST database from Sorghum: dark-grown seedlings  
Unpublished (2000)  
Contact: Cord M. Pratt M  
The University of Georgia  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Fax: 706 542 1805  
Email: mpratt@uga.edu  
Small: mpratt@uga.edu  
below: mpratt@uga.edu  
is 30 Phred quality 16. The threshold for highest quality sequence  
Seq primer: PolyMx  
High quality sequence start: 30  
High quality sequence stop: 638  
POLY-NO.

Location/Qualifiers  
/organism="Sorghum bicolor"  
/dbref="taxon:4308"  
/note="Organ: 5-day-old dark-grown seedlings; Vector:  
Lambda Zap; Site: 1. XhoI; Site: 2. EcoRI; The library was  
made from poly-A RNA in the Clontech vector Lambda ZAP II."



















SOURCE soybean  
ORGANISM Glycine max

REFERENCE  
AUTHORS Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Charophyta; Equisetum; Gymnosperms; Angiosperms; Core eudicots; Rosidae; Eumecostematales; Fabales; Papilionales; Phaseolaceae; Glycine.

FILES (bases 1 to 576)  
A. R. Bolla B., Maria M., Hillier L., Knecht J., Corvelli V., Khanna Wylie P., Underwood K., Stephens M., Thaisang B., Allen M., Bowers J., Schaefer M., Schaefer M., Schaefer M., Schaefer M., Schaefer M., R. R. Ritter E., Kohn S., Slight J., Jackson J., Cardenas W., Mcdonnell R., Waterson R. and Wilson R.

FILE JOURNAL  
UNPUBLISHED PROJECT  
Contact: Shoemaker B/Public Soybean EST Project  
Public Soybean EST Project  
444 Forest Park Parkway, Box 8301, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1800  
Email: eststation.wustl.edu

COMMENT This clone is available through ResGen, Invitrogen Corp. 2130  
California Avenue, Carlsbad, CA 92008. For further information  
call: (800) 531-4363 or contact via email: eststation.com  
Seq primer: -40R from Gibco  
High quality sequence (top): 40.  
1..576  
/organism="Glycine max"  
/clone\_lib="Gm-cl049"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl049-2643"  
/new\_stage="3 week old"  
/lab\_host="DH10B"  
/xhoi="The Clontech Pluscript II RFL Site 1, BORI: Site 2  
by Dr. J. Specht, University of Nebraska (Shoemaker and  
Shoemaker 1995). The cDNA library was constructed from mRNA  
isolated from developing green pods of the soybean plant  
grown plants. Complementary DNA was synthesized from mRNA  
using a primer consisting of a poly(dT) sequence with a  
3' BamHI site. The cDNA fragments were directionally cloned  
ligated to the blunt-ended cDNA fragments followed by XhoI  
digestion. The cDNA fragments were directionally cloned  
into the pGEMT vector. The library was constructed into  
DH10B host cells (GibcoBRL). The library was constructed  
into the pGEMT vector. Dr. Paul Keim's laboratory at Northern  
Arlington, VA.

BASE COUNT 185 a 100 c 130 g 161 t

Query Match 22.3k; Score 271; DB 10; Length 576;  
Best Local Similarity 70.6k; Pred. No. 3e-30;  
Matches 361; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

Db 393 TGAAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 452  
Oy 44 TAAAGTGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 452

Oy 453 GCTATTTGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 512  
Db 104 GCTATTTGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 512

Oy 513 TACAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 572  
Db 343 TACAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 572

Oy 164 TACAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 572  
Db 164 TACAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 572

Oy 573 ATTCAGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 632  
Db 573 ATTCAGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 632

Oy 224 ACTCCAGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 628  
Db 224 ACTCCAGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 628

Oy 633 GAGATTGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 692  
Db 284 GAGATTGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 692

Oy 693 AAGATCTTGGATGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 752  
Db 344 AAGATCTTGGATGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 752

Oy 344 CTAAGCTCTGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 812  
Db 404 CTAAGCTCTGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 812

Oy 813 ATTCAGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 872  
Db 404 ATTCAGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 872

Oy 454 ATTCAGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 932  
Db 454 ATTCAGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 932

Oy 873 GCGAGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 992  
Db 524 GCGAGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 992

RESULT 15  
AN056154 564 bp mRNA linear EST 27-SEP-1999  
DEFINITION mRNA sequence.  
ACCESSION AN056154.1 GI:5928862  
VERSION AN056154.1  
KEYWORDS EST  
SOURCE Soybean.  
ORGANISM Glycine max.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Charophyta; Equisetum; Gymnosperms; Angiosperms; Core eudicots; Rosidae; Eumecostematales; Fabales; Papilionales; Phaseolaceae; Glycine.  
1 (bases 1 to 564)  
/lab\_host="DH10B"  
/xhoi="The Clontech Pluscript II RFL Site 1, BORI: Site 2  
by Dr. J. Specht, University of Nebraska (Shoemaker and  
Shoemaker 1995). The cDNA library was constructed from mRNA  
isolated from developing green pods of the soybean plant  
grown plants. Complementary DNA was synthesized from mRNA  
using a primer consisting of a poly(dT) sequence with a  
3' BamHI site. The cDNA fragments were directionally cloned  
ligated to the blunt-ended cDNA fragments followed by XhoI  
digestion. The cDNA fragments were directionally cloned  
into the pGEMT vector. The library was constructed into  
DH10B host cells (GibcoBRL). The library was constructed  
into the pGEMT vector. Dr. Paul Keim's laboratory at Northern  
Arlington, VA.

BASE COUNT 124 a 166 c 170 g 102 t 2 others

Query Match 22.0k; Score 268; DB 9; Length 564;  
Best Local Similarity 69.2k; Pred. No. 6.2e-30;  
Matches 364; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

Oy 508 ATGATAGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 567  
Db 3 AGATAGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 567

Oy 568 GTTCATGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 627  
Db 568 GTTCATGAGGAGCTCTGATATGACATCTGGATGACATATTTATGACCAATT 627

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Db 63 CTCTGCGAGAGGACCTACGTACGTCTGTGAGCGACACCTCTGAGGACCGGGCT 122
OY 628 AATATAGATTATAGCTTTAGTCGAGAGACCTGTGCGAAMATATACGAGAGTGTGTGA 687
Db 123 GACACGACCTCTACCTTGGAGATCAGACGACGACGCGCGACGACATNCSGAGATAGGCA 182
OY 688 AGTGGCAAGCTTTTGTGCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGAT 747
Db 183 AGNAGCGAGCTTTGTGCGACCTGTGCGATGCGATGCGATGCGATGCGATGCGAT 242
OY 748 CAGGAGATGCGAGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGAT 807
Db 243 CAGAGCGACGAGAGCGGTGTGCGATGCGATGCGATGCGATGCGATGCGATGCGAT 302
OY 808 TATTGATTGCGCGCTAAMATTTGTGAGCTGTGATCTTAAGGCGCTATACAGCTTGC 867
Db 303 CTGTGAGCTGCGCTTCAAGTGTGCGAGCGAGGACCCAGAGGCGCTACAGAGCTTGC 362
OY 868 ACTTACAGAGAGATTAAAGCTTCTCAGGATTTGATGATCATACGACACCGAATTA 927
Db 363 AGCGCGCGAGATGAGAGGTTCTGCGATGCGATGCGATGCGATGCGATGCGATGCGAT 422
OY 928 TGTGAGATGATTAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 987
Db 423 CTTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482
OY 988 GGAAGTTATGCTTACTTGTGAGAGAGATTTTGTGAGCTTAT 1033
Db 483 TCAAGTTGTCTGCTTACTTGTGAGAGATGCTTGTCTGTGAGACTAG 528

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Search completed: November 2, 2002, 00:53:18  
 Job time : 1737 secs



Genome version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2002, 00:28:47 / Search time 50 Seconds  
761.966 Million cell updates/sec

Title: US-09-720-384a-4  
Sequence: 1896  
Perfected score: 1 RPHFIMTIPVITVQDP.....PKMAKVCTLEENLQA 343

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 11077936 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A\_Genescap\_032802.\*

- 1: /S1081/gcdatg/genescap/genescap-emb1/AA1980.DAT.\*
- 2: /S1081/gcdatg/genescap/genescap-emb1/AA1981.DAT.\*
- 3: /S1081/gcdatg/genescap/genescap-emb1/AA1982.DAT.\*
- 4: /S1081/gcdatg/genescap/genescap-emb1/AA1983.DAT.\*
- 5: /S1081/gcdatg/genescap/genescap-emb1/AA1984.DAT.\*
- 6: /S1081/gcdatg/genescap/genescap-emb1/AA1985.DAT.\*
- 7: /S1081/gcdatg/genescap/genescap-emb1/AA1986.DAT.\*
- 8: /S1081/gcdatg/genescap/genescap-emb1/AA1987.DAT.\*
- 9: /S1081/gcdatg/genescap/genescap-emb1/AA1988.DAT.\*
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- 22: /S1081/gcdatg/genescap/genescap-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	1636	100.0	343	21	AA144789			Corn Adenylylsulphate kinase-2
2	887	48.6	224	21	AA144788			Wheat Adenylylsulphate kinase-2
3	859	47.9	246	21	AA144792			Wheat Adenylylsulphate kinase-2
4	834	45.7	208	21	AA135768			Arabidopsis thaliana
5	834	45.7	208	21	AA135768			Arabidopsis thaliana
6	817	44.7	259	21	AA134477			Arabidopsis thaliana
7	817	44.7	259	21	AA134477			Arabidopsis thaliana
8	816	44.7	251	21	AA110107			Arabidopsis thaliana
9	816	44.7	251	21	AA138348			Arabidopsis thaliana
10	816	44.7	263	21	AA110106			Arabidopsis thaliana
11	816	44.7	263	21	AA138347			Arabidopsis thaliana

12	816	44.7	276	21	AA110105			Arabidopsis thaliana
13	816	44.7	276	21	AA110105			Arabidopsis thaliana
14	814	44.6	236	21	AA144478			Arabidopsis thaliana
15	809	44.3	237	21	AA133120			Arabidopsis thaliana
16	777	42.6	293	21	AA171957			Arabidopsis thaliana
17	777	42.6	293	21	AA171957			Arabidopsis thaliana
18	757	41.5	252	21	AA147458			A. thaliana enviro
19	757	41.5	252	21	AA147458			Arabidopsis thaliana
20	757	41.5	310	21	AA147456			Arabidopsis thaliana
21	752.5	41.2	252	21	AA14580			Arabidopsis thaliana
22	752.5	41.2	252	21	AA14580			Arabidopsis thaliana
23	752.5	41.2	305	21	AA14579			Arabidopsis thaliana
24	617	33.8	161	21	AA133456			Arabidopsis thaliana
25	495	27.1	624	19	AA107094			Human disease rela
26	495	27.1	624	19	AA107094			Human disease rela
27	495	27.1	625	20	AA107882			Human secreted pro
28	492.5	27.0	648	22	AA124348			Novel human secret
29	489	26.8	210	21	AA144789			Arabidopsis thaliana
30	489	26.8	210	21	AA144789			Arabidopsis thaliana
31	474	26.0	619	21	AA179214			Human transferrin
32	435.5	23.8	635	22	AA171650			Drosophila melanog
33	435.5	23.8	635	22	AA171650			Drosophila melanog
34	390	21.4	151	21	AA148310			Arabidopsis thaliana
35	390	21.4	151	21	AA148310			Arabidopsis thaliana
36	325.5	17.6	148	21	AA12628			Arabidopsis thaliana
37	226.5	14.0	148	21	AA12628			Arabidopsis thaliana
38	249	13.6	58	21	AA147793			zeas myos protein f
39	202.5	11.1	65	22	AA140286			Wheat Adenylylsulph
40	202.5	11.1	65	22	AA140286			Peptide 16622 enco
41	202.5	11.1	65	22	AA161056			Human brain expres
42	202.5	11.1	65	22	AA13760			Human bone marrow
43	130.5	6.2	160	21	AA122534			S. lavendulae MGU
44	130.5	6.2	160	21	AA122534			S. lavendulae MGU
45	117	6.4	361	22	AA134709			Human protein sequ

## ALIGNMENTS

RESULT 1  
AA144789  
AA144789 standard; Protein; 343 aa.  
XX AA144789;  
AC AC  
DT 04-MAY-2000 (first entry)  
XX

Corn Adenylylsulphate kinase-2.

Adenylylsulphate kinase; Adenosine-5'-phosphosulphate kinase; APS Kinase;

3'-Phospho-adenosine-5'-phosphosulphate; PAP5; sulphate assimilation;

corn; clone p0016.ctc5c40rb; transgenic plant; screen; antibody.

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XX Claim 6: Page 31-32: 42pp: English.

XX The present sequence is the corn adenylylsulphate kinase (APS kinase),

XX clone p0016:ctac42b, derived from corn pooled tassel shoots, p0016.com

XX cDNA library, this has 52k sequence identity to *Catharanthus roseus* APS

XX kinase (AF088510) and 70% sequence identity to *Catharanthus roseus* APS

XX the conversion of adenosine-5' phosphosulphate (APS) to 3'-phospho-

XX adenosine-5' phosphosulphate (pAPS). The nucleotide sequence is used as

XX a primer to identify, obtain and synthesize sulphate assimilation

XX proteins from other plants. It is also used to produce transgenic plants

XX of a sulphate assimilation protein. The APS kinase peptides are useful for

XX producing antibodies, that are used to screen and isolate cDNA clones.

XX Sequence 343 AA:

Query Match 100.0%: Score 1826; DB 21; Length 343;

Best Local Similarity 100.0%; Pred. No. 7.9e-172; Mismatches 0; Indels 0; Gaps 0;

XX 1 REFNPETVITQTFSPSPASQSQDQNTLLPPTLLAVLNQRPAPVWG 60

XX 61 LPTSDANIPALVNLGTPSSHSAGLSGREGREGARPTGIRGIVGMYRRNG 120

XX 121 AACPENSHPEKPEKPMNCKSTNLLHNLNCLQSDQKLLQGCQVYVITGLSSGKS 180

XX 181 ACPGASHSPVEKPMNCKSTNLLHNLNCLQSDQKLLQGCQVYVITGLSSGKS 180

XX 182 TLACALSHELKRGHLYTVLDGNIHRLGDSFKADPRAENTRGEVAKLPADAGYI 240

XX 241 CIASLSYPRDRDCAALLPHNFTVEFDLPFLICDAPGKGLKLPATCKIKGFTGL 300

XX 301 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 343

XX 302 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 343

RESULT 2

XX AN44788

XX AN44788 standard; Protein: 224 AA.

XX AC AC AN44788;

XX DT DT 04-MAY-2000 (first entry)

XX DE DE Corn Adenylylsulphate kinase-1.

XX KW KW Adenylylsulphate kinase; Adenosine-5' phosphosulphate kinase; APS kinase;

XX KW 3'-phospho-adenosine-5' phosphosulphate; pAPS; sulphate assimilation;

XX KW corn clone ctmn:p0086.b10; transgenic plant; screen; antibody.

XX ZOO ZOO ZOO mays.

XX PR PR W0200004165-AL.

XX XX 27-JAN-2000.

XX PD PD 13-JUL-1995; 99MO-US1809.

XX PF PF 14-JUL-1998; 98US-009283.

XX XX 14-JUL-1998; 98US-009283.

XX XX (DUPO) DU PONT DE NEMOURS & CO E.I.

XX Falco SC, Allen SM, Anderson SL;

XX WPI: 2000-182430/16.

XX N-P808; AM500159.

XX New nucleic acid molecule and chimeric gene encoding an adenosine-5' phosphosulphate kinase, useful for altering expression of sulfate assimilation protein in plants -

XX Claim 6: Page 29-30; 42pp: English.

XX The present sequence is the corn adenylylsulphate kinase (APS kinase),

XX also known as adenosine-5' phosphosulphate kinase. It is obtained from

XX this corn clone p0016:ctac42b, derived from corn pooled tassel shoots, p0016.com

XX This sequence has 52% identity to *Catharanthus roseus* APS kinase (AF088510)

XX and 70% sequence identity to *Catharanthus roseus* APS kinase (AF088510)

XX The conversion of adenosine-5' phosphosulphate (APS) to 3'-phospho-

XX adenosine-5' phosphosulphate (pAPS). The nucleotide sequence is used as

XX a primer to identify, obtain and synthesize sulphate assimilation

XX proteins from other plants. It is also used to produce transgenic plants

XX of a sulphate assimilation protein. The APS kinase peptides are useful for

XX producing antibodies, that are used to screen and isolate cDNA clones.

XX Sequence 224 AA:

Query Match 100.0%: Score 887; DB 21; Length 224;

Best Local Similarity 77.0%; Pred. No. 2.8e-79; Mismatches 17; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

XX 121 AACPENSHPEKPEKPMNCKSTNLLHNLNCLQSDQKLLQGCQVYVITGLSSGKS 180

XX 181 TLACALSHELKRGHLYTVLDGNIHRLGDSFKADPRAENTRGEVAKLPADAGYI 240

XX 241 CIASLSYPRDRDCAALLPHNFTVEFDLPFLICDAPGKGLKLPATCKIKGFTGL 300

XX 301 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 302 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 303 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 304 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 305 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 306 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 307 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 308 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 309 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 310 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 311 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 312 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 313 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 314 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 315 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 316 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 317 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 318 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 319 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 320 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 321 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 322 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 323 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 324 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 325 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 326 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 327 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 328 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 329 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 330 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 331 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 332 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 333 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 334 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 335 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 336 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 337 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 338 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 339 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 340 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 341 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 342 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 343 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 344 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 345 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 346 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 347 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 348 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 349 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

XX 350 DQPTPEPPNGSEIVTKMDQECSPKAMKQVLTLENNQIA 342

RESULT 2

XX AN44792

XX AN44792 standard; Protein: 246 AA.

XX AC AC AN44792;

XX DT DT 04-MAY-2000 (first entry)

XX DE DE Wheat Adenylylsulphate kinase-1.

XX KW KW Adenylylsulphate kinase; Adenosine-5' phosphosulphate kinase; APS kinase;

XX KW 3'-phospho-adenosine-5' phosphosulphate; pAPS; sulphate assimilation;

XX KW wheat clone wpi:FA0101.62; transgenic plant; screen; antibody.

XX ZOO ZOO ZOO Triticum aestivum.

XX PR PR W0200004165-AL.

XX XX 27-JAN-2000.

XX PD PD 13-JUL-1995; 99MO-US1809.

XX PF PF 14-JUL-1998; 98US-009283.

XX XX 14-JUL-1998; 98US-009283.

XX XX (DUPO) DU PONT DE NEMOURS & CO E.I.



PI Falco SC, Allen SM, Anderson SL;  
 DR N-FS08: 2000-182430/16.  
 DR N-FS08: AA250163.  
 PT New nucleic acid molecule and chimeric gene encoding an adenosine-5'-  
 phosphosulphate kinase, useful for altering expression of sulfate  
 PT assimilation protein in plants -  
 XX Claim 6: Page 35; 42pp; English.  
 XX The present sequence is the wheat adenylsulphate kinase (APS kinase),  
 CC also known as adenosine-5' phosphosulphate kinase. This is obtained  
 CC from clone w1-pk01142, derived from 7 day old light grown wheat root  
 CC tissue. This sequence has 6A sequence identity to  
 CC characterising mouse APS Kinase. This sequence is a full length  
 CC protein, that catalyses the conversion of adenosine-5' phosphosulphate  
 CC (APS) to 3'-phospho-adenosine-5' phosphosulphate (PAPS). The nucleotide  
 CC sequence is identical to the sequence of the APS kinase from Arabidopsis  
 CC synthesise sulphate assimilation proteins from other plants. It is also  
 CC used to produce transgenic plants, that are useful for altering the  
 CC sulphate levels in plants. The present sequence is also used to produce  
 CC peptides are useful for producing antibodies, that are used to screen  
 CC and isolate cDNA clones.  
 XX Sequence 246 AA;  
 XX Query Match Similarity 47.0%; Score 856; DB 21; Length 246;  
 XX M161; Conservative: 76; Ident: 24; Mismatches: 25; Indels 0; Gaps 0;  
 OY 133 EKPMSNIGSTNINWCLDQSDKILQDQKQVWITGLSSGSGSTLACSLREILIC 192  
 DB 36 DLKVTSTVQKSTNINWCLDQSDKILQDQKQVWITGLSSGSGSTLACSLREILIC 95  
 OY 193 RHLITVYLDGMLRHGLNDLSPFAEDPAENTPRGVKMLPANDGVICIASLSPYRD 252  
 DB 96 RHLITVYLDGMLRHGLNDLSPFAEDPAENTPRGVKMLPANDGVICIASLSPYRD 155  
 DB 96 RHLITVYLDGMLRHGLNDLSPFAEDPAENTPRGVKMLPANDGVICIASLSPYRD 155  
 OY 253 RDCAALLPMSITFETDLPKICEDAPRGKGLKARQKIGFTGDDPYEPINRGI 312  
 DB 156 RSARLLKLSITFETDLPKICEDAPRGKGLKARQKIGFTGDDPYEPINRGI 215  
 OY 313 VIKMDQDTPSKANAKOVLTLENGTQ 342  
 DB 216 VIOCHAGCATSKANOVLTLENGTQ 245

RESULT 4  
 AA044791  
 ID AA044791 standard; Protein: 311 AA.  
 AC AA044791;  
 XX 04-MAY-2000 (first entry)  
 XX Soybean Adenylsulphate kinase.  
 DE Adenylsulphate kinase; Adenosine-5-phosphosulphate kinase; APS kinase;  
 KM 3'-phospho-adenosine-5' phosphosulphate; PAPS; sulphate assimilation;  
 KM soybean; clone apd2c:pk013.all; transgenic plant; screen; antibody.  
 CS Glycine max.  
 XX W0200004165-AL.  
 XX 27-JAN-2000.  
 PD 13-JUL-1999; 99NO-0815809.  
 XX 13-JUL-1999; 98US-0092833.  
 PR 09-MAY-1999; 98US-0125945.  
 PR 09-MAY-1999; 98US-0125945.

XX Falco SC, Allen SM, Anderson SL;  
 XX WPI: 2000-182430/16.  
 DR N-FS08: AA250162.  
 PT New nucleic acid molecule and chimeric gene encoding an adenosine-5'-  
 phosphosulphate kinase, useful for altering expression of sulfate  
 PT assimilation protein in plants -  
 XX Claim 6: Page 33-34; 42pp; English.  
 XX The present sequence is the soybean adenylsulphate kinase (APS kinase),  
 CC also known as adenosine-5' phosphosulphate kinase. This is obtained from  
 CC clone apd2c:pk013.all, derived from soybean developing pods. apd2c cDNA  
 CC sequence is identical to the sequence of the APS kinase from Arabidopsis  
 CC kinase. APS kinase is a sulphate assimilation protein, that catalyses  
 CC the conversion of adenosine-5' phosphosulphate (APS) to 3'-phospho-  
 CC adenosine-5' phosphosulphate (PAPS). The nucleotide sequence is identical  
 CC to the sequence of the APS kinase from Arabidopsis. This sequence is used as  
 CC a probe and primer to identify and isolate cDNA clones.  
 CC This sequence is also used to produce transgenic plants, that are useful for  
 CC altering the sulphate levels in plants. The present sequence is also used to  
 CC produce peptides are useful for producing antibodies, that are used to screen  
 CC and isolate cDNA clones.  
 XX Sequence 311 AA;  
 XX Query Match Similarity 45.7%; Score 852; DB 21; Length 311;  
 XX M153; Conservative: 31; Ident: 26; Mismatches: 23; Indels 0; Gaps 0;  
 OY 137 MSVSGSTNINWCLDQSDKILQDQKQVWITGLSSGSGSTLACSLREILIC 196  
 DB 105 MSVSGSTNINWCLDQSDKILQDQKQVWITGLSSGSGSTLACSLREILIC 164  
 OY 197 TVYLDGMLRHGLNDLSPFAEDPAENTPRGVKMLPANDGVICIASLSPYRD 256  
 DB 165 STLDGMLRHGLNDLSPFAEDPAENTPRGVKMLPANDGVICIASLSPYRD 224  
 OY 257 RALLPMSITFETDLPKICEDAPRGKGLKARQKIGFTGDDPYEPINRGI 316  
 DB 225 RALLPMSITFETDLPKICEDAPRGKGLKARQKIGFTGDDPYEPINRGI 284  
 OY 317 KQDCTSPKAKAKOVLTLENGTQ 343  
 DB 285 KQDCTSPKAKAKOVLTLENGTQ 311

RESULT 5  
 AA035788  
 ID AA035788 standard; Protein: 208 AA.  
 AC AA035788;  
 XX 18-OCT-2000 (first entry)  
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 43769.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 43769.  
 KM Protein identification; signal transduction pathway; metabolic pathway;  
 KM hydrolase; gene expression; genetic mapping; gene expression control; promoter;  
 KM termination sequence.  
 CS Arabidopsis thaliana.  
 XX EP103405-A2.  
 XX 06-SEP-2000.  
 PD 25-FEB-2000; 2000EP-0310439.  
 XX 25-FEB-1999; 99US-0121825.  
 PR 25-FEB-1999; 99US-0121825.  
 PR 09-MAY-1999; 98US-0125945.  
 PR 09-MAY-1999; 98US-0125945.

PR	23-MAR-1991	99US-012578R
PR	23-MAR-1991	99US-012626A
PR	29-MAR-1991	99US-012678S
PR	29-MAR-1991	99US-012765S
PR	05-APR-1991	99US-012803A
PR	05-APR-1991	99US-012833A
PR	06-APR-1991	99US-012871A
PR	06-APR-1991	99US-012871A
PR	19-APR-1991	99US-013007R
PR	19-APR-1991	99US-013007R
PR	21-APR-1991	99US-013044S
PR	21-APR-1991	99US-013044S
PR	23-APR-1991	99US-013051O
PR	23-APR-1991	99US-013051O
PR	28-APR-1991	99US-013114S
PR	28-APR-1991	99US-013114S
PR	04-MAY-1991	99US-013268A
PR	04-MAY-1991	99US-013268A
PR	05-MAY-1991	99US-013246S
PR	05-MAY-1991	99US-013246S
PR	06-MAY-1991	99US-013248S
PR	06-MAY-1991	99US-013248S
PR	07-MAY-1991	99US-013286J
PR	07-MAY-1991	99US-013286J
PR	11-MAY-1991	99US-0134256
PR	11-MAY-1991	99US-0134256
PR	14-MAY-1991	99US-013417S
PR	14-MAY-1991	99US-013417S
PR	14-MAY-1991	99US-0134221
PR	14-MAY-1991	99US-0134221
PR	15-MAY-1991	99US-013476S
PR	15-MAY-1991	99US-013476S
PR	19-MAY-1991	99US-013494I
PR	19-MAY-1991	99US-013494I
PR	20-MAY-1991	99US-013512A
PR	20-MAY-1991	99US-013512A
PR	24-MAY-1991	99US-013562S
PR	24-MAY-1991	99US-013562S
PR	25-MAY-1991	99US-013602I
PR	25-MAY-1991	99US-013602I
PR	26-MAY-1991	99US-013678J
PR	26-MAY-1991	99US-013678J
PR	01-JUN-1991	99US-013742Z
PR	01-JUN-1991	99US-013742Z
PR	02-JUN-1991	99US-013752S
PR	02-JUN-1991	99US-013752S
PR	07-JUN-1991	99US-013772A
PR	07-JUN-1991	99US-013772A
PR	08-JUN-1991	99US-013809A
PR	08-JUN-1991	99US-013809A
PR	10-JUN-1991	99US-013864T
PR	10-JUN-1991	99US-013864T
PR	14-JUN-1991	99US-013911S
PR	14-JUN-1991	99US-013911S
PR	16-JUN-1991	99US-013945J
PR	16-JUN-1991	99US-013945J
PR	17-JUN-1991	99US-013949Z
PR	17-JUN-1991	99US-013949Z
PR	18-JUN-1991	99US-013954A
PR	18-JUN-1991	99US-013954A
PR	18-JUN-1991	99US-013956S
PR	18-JUN-1991	99US-013956S
PR	18-JUN-1991	99US-013945T
PR	18-JUN-1991	99US-013945T
PR	18-JUN-1991	99US-013949S
PR	18-JUN-1991	99US-013949S
PR	18-JUN-1991	99US-013946Z
PR	18-JUN-1991	99US-013946Z
PR	18-JUN-1991	99US-013946J
PR	18-JUN-1991	99US-013946J
PR	21-JUN-1991	99US-013969R
PR	21-JUN-1991	99US-013969R
PR	23-JUN-1991	99US-014035A
PR	23-JUN-1991	99US-014035A
PR	24-JUN-1991	99US-014082J
PR	24-JUN-1991	99US-014082J
PR	26-JUN-1991	99US-014026S
PR	26-JUN-1991	99US-014026S
PR	06-JUL-1991	99US-014260J
PR	06-JUL-1991	99US-014260J
PR	12-JUL-1991	99US-014277R
PR	12-JUL-1991	99US-014277R
PR	13-JUL-1991	99US-014334Z
PR	13-JUL-1991	99US-014334Z
PR	15-JUL-1991	99US-014400S
PR	15-JUL-1991	99US-014400S
PR	16-JUL-1991	99US-014401S
PR	16-JUL-1991	99US-014401S
PR	02-AUG-1991	99US-014513R
PR	02-AUG-1991	99US-014513R
PR	23-SEP-1991	99US-015248E
PR	23-SEP-1991	99US-015248E
PR	24-SEP-1991	99US-015365S
PR	24-SEP-1991	99US-015365S
PR	29-SEP-1991	99US-015659E
PR	29-SEP-1991	99US-015659E
PR	04-OCT-1991	99US-015711T
PR	04-OCT-1991	99US-015711T
PR	06-OCT-1991	99US-015782S
PR	06-OCT-1991	





Hybridization assay; genetic mapping; gene expression control; promoter;  
 termination sequence.

US Arabidopsis thaliana.

PR EPI03405-A2.

XX 06-SEP-2000.

XX 25-FEB-2001; 200HP-0.01439.

PR 05-MAR-1999; 99US-021825.

PR 09-MAR-1999; 99US-013180.

PR 25-MAR-1999; 99US-023548.

PR 25-MAR-1999; 99US-016264.

PR 29-MAR-1999; 99US-016785.

PR 06-APR-1999; 99US-028234.

PR 08-APR-1999; 99US-0128714.

PR 19-APR-1999; 99US-010845.

PR 21-APR-1999; 99US-0130445.

PR 23-APR-1999; 99US-030510.

PR 28-APR-1999; 99US-013449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132486.

PR 05-MAY-1999; 99US-012485.

PR 06-MAY-1999; 99US-012486.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-013419.

PR 14-MAY-1999; 99US-0134221.

PR 18-MAY-1999; 99US-0134760.

PR 19-MAY-1999; 99US-0134941.

PR 21-MAY-1999; 99US-0135124.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 04-JUN-1999; 99US-0137503.

PR 07-JUN-1999; 99US-0137724.

PR 09-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138147.

PR 14-JUN-1999; 99US-0139119.

PR 15-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139500.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140855.

PR 29-JUN-1999; 99US-0140951.

PR 30-JUN-1999; 99US-0141267.

PR 01-JUL-1999; 99US-0141842.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142380.

PR 09-JUL-1999; 99US-0142820.

PR 12-JUL-1999; 99US-0142877.

PR 14-JUL-1999; 99US-0143244.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144066.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.

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PR 20-JUL-1999; 99US-0144352.

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PR 20-AUG-1999; 99US-0149629;
PR 20-AUG-1999; 99US-0149629;
PR 23-AUG-1999; 99US-0148902;
PR 23-AUG-1999; 99US-0148902;
PR 25-AUG-1999; 99US-0150565;
PR 25-AUG-1999; 99US-0150565;
PR 26-AUG-1999; 99US-0150884;
PR 26-AUG-1999; 99US-0150884;
PR 27-AUG-1999; 99US-0150615;
PR 27-AUG-1999; 99US-0150860;
PR 30-AUG-1999; 99US-0151103;
PR 30-AUG-1999; 99US-0151103;
PR 01-SEP-1999; 99US-0151390;
PR 01-SEP-1999; 99US-0151390;
PR 07-SEP-1999; 99US-0152363;
PR 10-SEP-1999; 99US-0153070;
PR 13-SEP-1999; 99US-0153758;
PR 13-SEP-1999; 99US-0153758;
PR 15-SEP-1999; 99US-0154018;
PR 15-SEP-1999; 99US-0154018;
PR 20-SEP-1999; 99US-0154779;
PR 20-SEP-1999; 99US-0154779;
PR 22-SEP-1999; 99US-0155139;
PR 22-SEP-1999; 99US-0155139;
PR 24-SEP-1999; 99US-0155456;
PR 24-SEP-1999; 99US-0155456;
PR 28-SEP-1999; 99US-0156458;
PR 28-SEP-1999; 99US-0156458;
PR 29-SEP-1999; 99US-0157596;
PR 29-SEP-1999; 99US-0157596;
PR 05-OCT-1999; 99US-0157753;
PR 05-OCT-1999; 99US-0157753;
PR 06-OCT-1999; 99US-0157865;
PR 06-OCT-1999; 99US-0157865;
PR 08-OCT-1999; 99US-0158232;
PR 08-OCT-1999; 99US-0158232;
PR 12-OCT-1999; 99US-0158369;
PR 12-OCT-1999; 99US-0158369;
PR 13-OCT-1999; 99US-0159224;
PR 13-OCT-1999; 99US-0159224;
PR 13-OCT-1999; 99US-0159225;
PR 13-OCT-1999; 99US-0159225;
PR 14-OCT-1999; 99US-0159328;
PR 14-OCT-1999; 99US-0159328;
PR 14-OCT-1999; 99US-0159331;
PR 14-OCT-1999; 99US-0159331;
PR 18-OCT-1999; 99US-0159584;
PR 18-OCT-1999; 99US-0159584;
PR 21-OCT-1999; 99US-0160741;
PR 21-OCT-1999; 99US-0160741;
PR 21-OCT-1999; 99US-0160741;
PR 21-OCT-1999; 99US-0160741;
PR 21-OCT-1999; 99US-0160770;
PR 21-OCT-1999; 99US-0160770;
PR 21-OCT-1999; 99US-0160814;
PR 21-OCT-1999; 99US-0160814;
PR 22-OCT-1999; 99US-0160981;
PR 22-OCT-1999; 99US-0160981;
PR 22-OCT-1999; 99US-0160980;
PR 22-OCT-1999; 99US-0160980;
PR 25-OCT-1999; 99US-0161405;
PR 25-OCT-1999; 99US-0161405;
PR 25-OCT-1999; 99US-0161405;
PR 25-OCT-1999; 99US-0161405;
PR 26-OCT-1999; 99US-0161360;
PR 26-OCT-1999; 99US-0161360;
PR 26-OCT-1999; 99US-0161361;
PR 26-OCT-1999; 99US-0161361;
PR 28-OCT-1999; 99US-0161992;
PR 28-OCT-1999; 99US-0161992;
PR 28-OCT-1999; 99US-0161993;
PR 28-OCT-1999; 99US-0161993;
PR 29-OCT-1999; 99US-0162142;
PR 29-OCT-1999; 99US-0162142;
Query Match 44.3% Score 809.5; DB 21; Length 237;
Met Local Similarity 65.5%; Pred. No. 1,4e-71;
Matches 157; Conservative 28; Wamatches 24; Indels 29; Gaps 1;
Oy 137 M5TCKSTN1GMNKLGDSDNKLQDQCVWITGLSGSSTKLACLRHLKRLK 196
Oy 137 M5TCKSTN1GMNKLGDSDNKLQDQCVWITGLSGSSTKLACLRHLKRLK 196
Db 1 M5TCKSTN1GMNKLGDSDNKLQDQCVWITGLSGSSTKLACLRHLKRLK 60
Oy 137 M5TCKSTN1GMNKLGDSDNKLQDQCVWITGLSGSSTKLACLRHLKRLK 227
Oy 137 M5TCKSTN1GMNKLGDSDNKLQDQCVWITGLSGSSTKLACLRHLKRLK 227
Db 61 SEVAFLEADMGVTCIASLSPYRDEACBALLEHNSFTVPLKLTNPNKPLKICSDSLR 120
Oy 228 SEVAFLEADMGVTCIASLSPYRDEACBALLEHNSFTVPLKLTNPNKPLKICSDSLR 267
Db 121 SEVAFLEADMGVTCIASLSPYRDEACBALLEHNSFTVPLKLTNPNKPLKICSDSLR 160
Oy 288 LARXK1GKFTGIDDPETPEETVTKMKDECPSPKANKVCLYKERNYIQ 342
Oy 288 LARXK1GKFTGIDDPETPEETVTKMKDECPSPKANKVCLYKERNYIQ 342
Db 181 LARXK1GKFTGIDDPETPEETVTKMKDECPSPKANKVCLYKERNYIQ 235
Search completed: November 2, 2002, 01:50:51
Job time : 52 secs

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GenCore version 5.1.3

Copyright (c) 1993 - 2002 CompuGen Ltd.

ON protein - protein search, using sw model

Run on: November 2, 2002, 01:49:58, Search time 19 Seconds

without alignments

440-946 Million cell updates/sec

US-09-720-384a-4

Perfect score: 1826

Sequence: 1 RFFPIINTEPLVTHQPP.....PRAMAKVCLYENSTYQA 343

Scoring table:

BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 211528 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA\*

2 : /C3n2\_5/prodata/2/aa/6A/COMB pep.\*

3 : /C3n2\_5/prodata/2/aa/6A/COMB pep.\*

5 : /C3n2\_5/prodata/2/aa/6A/COMB pep.\*

6 : /C3n2\_5/prodata/2/aa/6A/COMB pep.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Length	DB ID	Description
1	502.5	610	2	US-08-879-561-10	Sequence 10, Appl
2	495.2	27.1	2	US-08-879-561-9	Sequence 9, Appl
3	495.2	624	2	US-08-879-561-9	Sequence 9, Appl
4	97.5	5.3	655	4 US-09-347-813-4	Sequence 4, Appl
5	96.5	5.3	650	4 US-09-442-100-11	Sequence 11, Appl
6	96.5	5.3	650	4 US-09-442-100-11	Sequence 11, Appl
7	96.5	5.3	949	4 US-09-196-387-10	Sequence 10, Appl
8	96.5	5.3	1377	4 US-09-196-387-2	Sequence 2, Appl
9	96.5	5.3	1377	4 US-09-196-387-2	Sequence 2, Appl
10	95.2	5.2	540	4 US-09-212-168-3	Sequence 3, Appl
11	95.2	5.2	540	4 US-09-212-168-3	Sequence 3, Appl
12	95.2	1548	1	US-08-463-092B-7	Sequence 7, Appl
13	94.5	5.2	1548	2 US-08-460-907B-7	Sequence 7, Appl
14	94.5	5.1	415	2 US-08-815-718-2	Sequence 2, Appl
15	91.5	5.0	635	1 US-07-832-855-2	Sequence 2, Appl
16	91.5	5.0	635	1 US-07-832-855-2	Sequence 2, Appl
17	89.5	4.9	221	2 US-08-704-311-43	Sequence 43, Appl
18	88.8	4.8	1271	1 US-08-095-734-2	Sequence 2, Appl
19	88.8	4.8	1271	1 US-08-441-623-2	Sequence 2, Appl
20	88.8	4.8	1271	1 US-08-441-623-2	Sequence 2, Appl
21	88.8	4.8	1271	4 US-09-342-163-2	Sequence 2, Appl
22	88.8	4.8	1271	5 PCT/0994-08667-2	Sequence 2, Appl
23	87.5	4.8	1487	2 US-08-760-489-2	Sequence 2, Appl
24	87.5	4.8	1487	2 US-08-760-489-2	Sequence 2, Appl
25	87.5	4.8	1487	2 US-09-185-773-2	Sequence 2, Appl
26	87.5	4.8	1487	2 US-09-185-773-2	Sequence 2, Appl
27	87.5	4.8	1487	4 US-09-185-773-4	Sequence 4, Appl

28	87	4.8	681	1	US-08-091-590A-18	Sequence 18, Appl
29	87	4.8	681	1	US-08-091-590A-18	Sequence 18, Appl
30	87	4.8	681	3	US-08-533-384-18	Sequence 18, Appl
31	87	4.8	1078	1	US-08-264-534-32	Sequence 32, Appl
32	87	4.8	1078	1	US-08-264-534-32	Sequence 32, Appl
33	87	4.8	1078	1	US-08-465-500-32	Sequence 32, Appl
34	87	4.8	1078	1	US-08-465-500-32	Sequence 32, Appl
35	87	4.8	1078	1	US-08-246-138-32	Sequence 32, Appl
36	87	4.8	1078	1	US-08-246-138-32	Sequence 32, Appl
37	87	4.8	1078	3	US-08-893-828-32	Sequence 32, Appl
38	86.5	4.7	2556	1	US-08-091-590A-20	Sequence 20, Appl
39	86.5	4.7	2556	1	US-08-533-384-18	Sequence 18, Appl
40	86.5	4.7	490	1	US-08-477-028A-10	Sequence 10, Appl
41	86.5	4.7	490	1	US-08-477-028A-10	Sequence 10, Appl
42	86.5	4.7	490	1	US-09-071-296-10	Sequence 10, Appl
43	86.5	4.7	490	1	US-09-071-296-10	Sequence 10, Appl
44	86.5	4.7	490	4	US-09-015-683-10	Sequence 10, Appl
45	85	4.7	163	4	US-09-191-988-10	Sequence 10, Appl
					US-09-191-988-10	Sequence 335, Appl

## ALIGNMENTS

RESULTS 10-561-10  
 : Sequence 10, Application US/08879561  
 : Patent No. 5617482  
 : GENETIC INFORMATION:  
 : APPLICANT: Hausman, Olga  
 : APPLICANT: Hillman, Jennifer L.  
 : APPLICANT: Hawkins, Philip R.  
 : APPLICANT: Hillman, Jennifer L.  
 : APPLICANT: Corley, Neil C.

: TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES  
 : INVENTOR: Hausman, Olga  
 : INVENTOR: Hillman, Jennifer L.  
 : INVENTOR: Hawkins, Philip R.  
 : INVENTOR: Hillman, Jennifer L.  
 : INVENTOR: Corley, Neil C.  
 : CORRESPONDENCE ADDRESS: 12  
 : ADDRESS: Incyte Pharmaceuticals, Inc.  
 : 9000 Rockledge Boulevard, Suite 200  
 : City, Palo Alto  
 : State, CA  
 : Country, USA

: COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : OPERATING SYSTEM: DOS  
 : SOFTWARE: FastSeq for Windows Version 2.0  
 : CURRENT APPLICATION DATA: 08/879,561  
 : FILING DATE: Herewith  
 : CLASSIFICATION: 424  
 : PRIORITY CLAIM: None  
 : APPLICATION NUMBER:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Bill  
 : REGISTRATION NUMBER: 36,749  
 : REFERENCE/DOCKET NUMBER: PP-0325 US  
 : TELEPHONE: 415-855-0555  
 : TELEFAX: 415-845-4166

: INFORMATION FOR SEQ ID NO: 10:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 610 amino acids  
 : TOPOLOGY: linear  
 : STRANDEDNESS: single  
 : FUNCTION: SOURCE: unknown  
 : CLONE: 705385  
 : US-08-879-561-10





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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA: US/09/196,387
: APPLICATION NUMBER: US/09/196,387
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: FILING DATE: June 10, 1998
: ATORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-343-1684
: INVENTOR: SEQ ID NO: 8
: SEQUENCE CHARACTERISTICS:
: LENGTH: 673 amino acids
: TYPE: amino acid
: MOLECULE TYPE: Protein
: US-09-196-387-8

Query Match 5.34; Score 96.5; Db 4; Length 673;
Best Local Similarity 20.24; Pred. No. 0.26;
Matches 78; Conservative 34; Mismatches 143; Indels 131; Gaps 15;

QY 4 HFTNTEPLVTHQPPSPAPGASQGGQNTLSPTFLAVILVNR----- 53
DB 13 HHQOGLAP-APGASAPPPPPPLSGCLAGTTPASFPASLAFSPHGLALPIDGGS 71
QY 54 -----APVLRLPTSD---APLVALVHGLTPRS 80
DB 72 RDPDRPSPDPVDTSCSTSTICTVAAPVAVPVAVTSAGAVNANGSINSSFS 131
QY 81 SHSAGLASGSRBGR-----EGKARTCHHGIGRWVRRRKGAAPGAPSPKYE 133
DB 132 SSPTSSSSSPSSPSSCAEPDAAGVSTALRPG-----AAGPTG----- 175
QY 134 KPMVNTCKFTNLMNCLTQSGDKQLLQKGVYVITLSSGSKSTLACALSRELICR 193
DB 176 VNAVSG--ALRELEACNDGNSVRYER-----VDANYNMADMGRKSSPLFA 223
QY 194 GHLYTVLQDNLRHGLMDLSFKADRAENIRRVGEVAFADAGVYCIASLISPYRDR 253
DB 224 A-----GPKGVYVHLLGANYHAGADGGDLPL-----H 254
QY 254 DACRALLPRLNFEVFDLPLICENDRPG-----LYKLARTCKIKGTFTI---D 301
DB 255 NAGS--FGHAEVYS-----LLQGGDNPANMKNNTTFLHAIKICKIDVCIQLHQA 306
QY 302 DPEPPIINSEVITMKDCEPSKAN 327
DB 307 DPNINTEGSKSLADAD---PSMAV 329

RESULT 7
US-09-196-387-10
: Sequence 10, Application US/09196387
: Patent No. 6277633
: GENERAL INFORMATION:
: APPLICANT: de Lange, Titia
: APPLICANT: Smith, Susan
: TITLE OF INVENTION: OF USE THEREOF
: NUMBER OF SEQUENCES: 12
: COMPILED BY: Klausner & Jackson
: ADDRESS: 411 Hackensack Avenue, 4th Floor
: STREET: 411 Hackensack Avenue, 4th Floor

```

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: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: CIP1: 0760
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA: US/09/196,387
: APPLICATION NUMBER: US/09/196,387
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: FILING DATE: June 10, 1998
: ATORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-343-1684
: INVENTOR: SEQ ID NO: 10
: SEQUENCE CHARACTERISTICS:
: LENGTH: 673 amino acids
: TYPE: amino acid
: MOLECULE TYPE: Protein
: US-09-196-387-10

Query Match 5.34; Score 96.5; Db 4; Length 949;
Best Local Similarity 20.24; Pred. No. 0.47;
Matches 78; Conservative 34; Mismatches 143; Indels 131; Gaps 15;

QY 4 HFTNTEPLVTHQPPSPAPGASQGGQNTLSPTFLAVILVNR----- 53
DB 13 HHQOGLAP-APGASAPPPPPPLSGCLAGTTPASFPASLAFSPHGLALPIDGGS 71
QY 54 -----APVLRLPTSD---APLVALVHGLTPRS 80
DB 72 RDPDRPSPDPVDTSCSTSTICTVAAPVAVPVAVTSAGAVNANGSINSSFS 131
QY 81 SHSAGLASGSRBGR-----EGKARTCHHGIGRWVRRRKGAAPGAPSPKYE 133
DB 132 SSPTSSSSSPSSPSSCAEPDAAGVSTALRPG-----AAGPTG----- 175
QY 134 KPMVNTCKFTNLMNCLTQSGDKQLLQKGVYVITLSSGSKSTLACALSRELICR 193
DB 176 VNAVSG--ALRELEACNDGNSVRYER-----VDANYNMADMGRKSSPLFA 223
QY 194 GHLYTVLQDNLRHGLMDLSFKADRAENIRRVGEVAFADAGVYCIASLISPYRDR 253
DB 224 A-----GPKGVYVHLLGANYHAGADGGDLPL-----H 254
QY 254 DACRALLPRLNFEVFDLPLICENDRPG-----LYKLARTCKIKGTFTI---D 301
DB 255 NAGS--FGHAEVYS-----LLQGGDNPANMKNNTTFLHAIKICKIDVCIQLHQA 306
QY 302 DPEPPIINSEVITMKDCEPSKAN 327
DB 307 DPNINTEGSKSLADAD---PSMAV 329

RESULT 8
US-09-196-387-2
: Sequence 10, Application US/09196387
: Patent No. 6277633
: GENERAL INFORMATION:
: APPLICANT: de Lange, Titia
: APPLICANT: Smith, Susan
: TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRT1 AND METHODS

```

1 TITLE OF INVENTION: QY USE THEREOF  
 2 NAME OF APPLICANT: US 09-720-384a-4  
 3 CORRESPONDENCE ADDRESS:  
 4 ADDRESSEE: Klüber & Jackson  
 5 CITY: Hackettsack Avenue, 4th Floor  
 6 CITY: Hackettsack  
 7 STATE: New Jersey  
 8 COUNTRY: USA  
 9 ZIP: 07601  
 10 COMPUTER READABLE FORM:  
 11 MEDIUM TYPE: floppy disk  
 12 MEDIUM TYPE: 5 1/4 inch floppy disk  
 13 OPERATING SYSTEM: PC-DOS/MS-DOS  
 14 SOFTWARE: PatentIn release #1.0, Version #1.30  
 15 COMPILATION: US/09/196,387  
 16 APPLICATION NUMBER: US/09/196,387  
 17 FILING DATE: 09/05/2002  
 18 PRIOR APPLICATION DATA:  
 19 APPLICATION NUMBER: 09/095,225  
 20 FILING DATE: June 10, 1998  
 21 AT: Jackson Eq., David A.  
 22 REGISTRATION NUMBER: 26,742  
 23 TELECOMMUNICATION INFORMATION:  
 24 TELEPHONE: 201-487-5800  
 25 TELEFAX: 201-443-1884  
 26 TELEX: 13351  
 27 INFORMATION FOR SEQ ID NO: 2:  
 28 SOURCE CHARACTERISTICS:  
 29 TYPE: amino acid  
 30 STRANDNESS: single  
 31 MOLECULE TYPE: protein  
 32 HYDROTHERMAL: NO

33 Query Match 5.3%, Score 96.5; DB 4; Length 1327;  
 34 Best Local Similarity 20.4%, Pred. No. 0.7;  
 35 Matches 79; Conservative 34; Mismatches 143; Indels 131; Gaps 15;

QY 4 RTNTELVITQTPSPAPASQDQGNLTSPITVAVLNQR-----53  
 DB 13 HQNQDLOP APASAPPPPPPLSPGLPPTTASTASGLAPSPHIGLALPGDGS 71  
 QY 54 -----APVRLRFTSD---APLVYHIGLTPRS 80  
 DB 72 REPGRSPSPDVGTCSTSTCTVAAPVYFVASTSAAGVAFAGSNNSSPS 131  
 QY 81 SHSGASLSDSRRGG-----RGGATKCHGLGRWRRHWGAQCTAPRPVKE 133  
 DB 132 SSSTSSSSSSSSSSSSSSSAPFANQVSTAPVGG-----AQDTG-----175  
 QY 134 KPVANIKGFTNHLNCLGSLQKGLQGVNLTGSLSGKSTLACALRELICR 193  
 DB 176 VFAVSG---ALHELLELSDNSVRYRL-----VDANNNKMDKRSKSPFLPA 223  
 QY 194 GHTLVTLGNDLRLHRLAFKADADANRVRVGVKALPALGATCTALSTPYRDR 253  
 DB 224 A-----GSMAGVDELLAGANNWAKDGGDGLP-----H 254  
 QY 254 DACRALPHSNTFVFDLPICRDPKQ-----LVKLAPRKIKFTGT---D 301  
 DB 255 NALS--FGLVATYS-----LLIQGQDNNADNNWNTPLHEATLGRIDNCLVLQRA 306  
 QY 302 DYTEPPINKEIVYKMDKDESPAM 327  
 DB 307 DPMINTDKSALAD---PRAAV 329

RESULT 9

US-09-884-072-3  
 Patent No. 582234  
 GENERAL INFORMATION:  
 ADDRESSEE: Klüber & Jackson  
 APPLICANT: Corley, Neil C.  
 CITY: Hackettsack Avenue, 4th Floor  
 CITY: Hackettsack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 MEDIUM TYPE: 5 1/4 inch floppy disk  
 OPERATING SYSTEM: DOS  
 SOFTWARE: PatentIn release #1.0, Version #1.30  
 COMPILATION: US/08/884,072  
 APPLICATION NUMBER: US/08/884,072  
 FILING DATE: Hackettsack  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,748  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4186  
 TELEX:

INFORMATION FOR SEQ ID NO: 3:  
 SOURCE CHARACTERISTICS:  
 TYPE: amino acid  
 STRANDNESS: single  
 MOLECULE TYPE: protein  
 IMMEDIATE SOURCE:  
 LIBRARY: BRAITUT13  
 US-08-884-072-3 1621777

Query Match 5.2%, Score 95; DB 2; Length 540;  
 Best Local Similarity 23.4%, Pred. No. 0.7;  
 Matches 52; Conservative 26; Mismatches 84; Indels 64; Gaps 13;

QY 1 RFPNTELVITQTPSPAPASQDQGNLTSPITVAVLNQR-----82  
 DB 34 RFPNTELVITQTPSPAPASQDQGNLTSPITVAVLNQR-----82  
 QY 49 WNDAPRPPVLTSD---APLP--ALVHIGLTPRS--SASGLAS--DSGRRGG 96  
 DB 83 ATQGLKPLKLEKRGVPLQGVATVAKELPGLQHPKMGAPFGQSHPEP 142  
 QY 97 RGGATKCHGLGRWRRHWGAQCTAPRPVKEVYKMDKDESPAM 149  
 DB 97 RGGATKCHGLGRWRRHWGAQCTAPRPVKEVYKMDKDESPAM 149  
 DB 143 ENNAAGVDELLAGANNWAKDGGDGLP-----H 193  
 QY 150 NCLGSGKSTLACALRELICR 195  
 DB 152 PHNLGSSSYHLFRQ-----GELTALGELGSSSYHLFRQ 226

RESULT 10  
 US-09-212-168-3  
 Sequence 3, Application US/09212168  
 Patent In Release  
 GENERAL INFORMATION:

1 APPLICANT: Baudman, Olga  
 2 APPLICANT: Corley, Neil C.  
 3 ATTORNEY/AGENT INFORMATION:  
 4 NAME: Billings, Lucy J. 710  
 5 REFERENCE/DOCKET NUMBER: RP-0333 US  
 6 TELECOMMUNICATION INFORMATION:  
 7 TELEPHONE: 415-855-0555  
 8 TELEFAX: 415-845-4166  
 9 TELEX:  
 10 INFORMATION FOR SEQ ID NO. 2:  
 11 SOURCE: Sequence  
 12 LENGTH: 540 amino acids  
 13 TYPE: amino acid  
 14 TRANSLATIONS: single  
 15 TOPOLOGY: linear  
 16 IMMEDIATE SOURCE:  
 17 LIBRARY: BRATUT13  
 18 IDENTIFICATION NUMBER: 021777

US-09-720-168-3

Query Match 5.24; Score 95; DB 4; Length 540;  
 Best Local Similarity 23.04; P-Val No. 0.27; Mismatches 52; Conservative 26; Mismatches 84; Indels 64; Gaps 13;

Oy 1 3RHHF---INTEPLHTTOPSPRAGSGORGNLLSPPTLAVIL 48

Db 34 RHHFVGTAAFPSPPLSLNPN---DHPOSSQGFPPFQSO---VPPFQSO--- 82

Oy 49 VNPQAPVPLGLTSD---APLP---ALVITGLTPSSH---SAGLAS---DSGRREG 96

Db 83 ATPLQKQLPALPAKGVPPQAPQAPLQKLSLQSNPKSKDPAPFQDSHP 142

Oy 97 EGRGATICH---RCGQVRRRRNCAAGCAPHSYKYSKYNSTGK---STNLIWH 149

Db 143 ESNNAKQAQQRQSQGH---GRLDGFPPS---REFPQAPLCLNMQAVTG 191

Oy 150 KCLIGDQRKGLQKQCVMTLQSGKSLTACALSRHCRH 195

Db 192 PNLQPSYSILTRQ-----GETLNLFLGTSCHSICH 226

RESULT 11

Sequence 7; Application US/084610928

GENERAL INFORMATION:

APPLICANT: Cole, Susan P.C.

ATTORNEY/AGENT INFORMATION:

TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING

TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS

1 NUMBER OF SEQUENCES: 9  
 2 CORRESPONDENCE ADDRESS:  
 3 APPLICANT: PARTED RESEARCH & DEVELOPMENT INNOVATIONS  
 4 ATTORNEY/AGENT INFORMATION:  
 5 NAME: Billings, Lucy J. 710  
 6 REFERENCE/DOCKET NUMBER: RP-0333 US  
 7 TELECOMMUNICATION INFORMATION:  
 8 TELEPHONE: 415-855-0555  
 9 TELEFAX: 415-845-4166  
 10 TELEX:  
 11 INFORMATION FOR SEQ ID NO. 1:  
 12 SOURCE: Sequence  
 13 LENGTH: 1548 amino acids  
 14 TYPE: amino acid  
 15 TRANSLATIONS: single  
 16 TOPOLOGY: linear  
 17 IMMEDIATE SOURCE:  
 18 LIBRARY: BRATUT13  
 19 IDENTIFICATION NUMBER: 021777

Query Match 5.24; Score 95; DB 1; Length 1548;  
 Best Local Similarity 23.04; P-Val No. 0.27; Mismatches 52; Conservative 26; Mismatches 84; Indels 64; Gaps 13;

Oy 65 DAPLPAVITPLTPIHSSACLASGSGREREPARTICRIGCRVRRRRNCAAP 124

Db 597 DASAASIAVSTVYMC---SQIVTDSQACG-----EKGVRBC 637

Oy 135 EANSRVEKSVSTKSTNLNMLNKLGSDKOKLQKQCVMTLQSGKSLAC 184

Db 638 DRYTOLSVSLRGL-----SLTPKQKLTWISTGSGKSLTG 678

Oy 195 AL-----SRELIHCGRHLYTGLDHLHNG---LNDLSFKASDRANRVRVEALP 236

Db 679 ALAMETSVESGEALWAKSTAYPOONMNTLKGTLFDEEAEQDQVRCOGL 738

Oy 237 AGVIC-----IASLISFYRR---DACAALPIENFTVDFLPLICANRKL 286

Db 739 LAQGLQGLTELRGQVNLGGQKARVSLAAY---FAMNYTLLQDLSALNVAQV 796

Oy 287 KLRATKRGKFTGI 300

Db 797 QGVTLGRKSTV 810



RESUME 12  
 US 08-440-907b-7  
 : Sequence 7, Application US/0846097b  
 : PAPER NO. 891720E  
 : CHAIRMAN: Desley, Roger G.  
 : APPLICANT: Cole, Susan P.C.  
 : TITLE OF INVENTION: FOR CONVERTING MULTIDRUG  
 : TITLE OF INVENTION: RESISTANCE ON A CELL  
 : NUMBER OF SOURCES: 9  
 : ADDRESS: PAPER RESEARCH & DEVELOPMENT INNOVATIONS  
 : STREET: Queen's University at Kingston  
 : CITY: Kingston  
 : STATE: Ontario  
 : COUNTRY: CANADA  
 : ZIP: K7L 3N6  
 : COMPUTER: IBM PC compatible  
 : SOFTWARE: IBM PC DOS/MS-DOS  
 : CURRENT APPLICATION DATA:  
 : FILING DATE: 05-JUN-1993  
 : PRIORITY APPLICATION DATA:  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION NUMBER: 07/966,933  
 : FILING DATE: 27-OCT-1992  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION NUMBER: 06/929,340  
 : FILING DATE: 6-MAR-1993  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/141,893  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION NUMBER: 08/407,207  
 : FILING DATE: 08-SEP-1995  
 : CLASSIFICATION: 424  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: JACKSON ESQ., DAVID A.  
 : TELEPHONE: (613) 545-5300  
 : TELEFAX: (613) 545-5300  
 : TELEPHONE: (613) 545-5300  
 : TELEFAX: (613) 545-5300  
 : NUMBER OF SEQ ID NO: 7  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1548 amino acids  
 : TYPE: amino acid  
 : MOLECULE TYPE: peptide  
 : FRAGMENT TYPE: internal  
 : ORGANISM: Homo sapiens

Query Match 5.2%; Score 95; DB 2; Length 1548;  
 Best Local Similarity 21.3%; Pred. No. 1.2;  
 Matches 34; Conservative 41; Mismatches 101; Indels 58; Gaps 8;  
 Db 595 DNASVAVSTVVMG-STGVTTDGAAG-----EGEVEES 617  
 Db 638 DREYQVLSKRLA-----SLTFPKLWIGTSGKSTLLG 678  
 Db 185 AL-----SEELCRULYTLVDQKLAH-LNGLSPKAEHRIKRVREVALEAD 236

Db 279 ALGEYSVESGEIAERSTAYVQWAMNATLGNLTFTDEHAEADQVIRCCQLEAD 738  
 Oy 273 ADVIC-----TASLISYRER-DKATALLHNSYEVTDKALICAKBPKGLY 286  
 Db 739 LAGPQGLGATGEGKGVMSGOKARSLARV--YANDVTLDDPISALDANGOREV 796  
 Oy 287 KLAETGKGTGTFQI 300  
 Db 797 QDVILGRJGRKTV 810  
 RESUME 13  
 US 08-906-865-3  
 : Sequence 3, Application US/08906865  
 : Patent No. 6040168  
 : CHAIRMAN: Greenard, Paul  
 : APPLICANT: Porton, Barbara  
 : TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE  
 : TITLE OF INVENTION: AND USES THEREOF  
 : ADDRESS: DAVID A. JACKSON, ESQ.  
 : STREET: 111 Hackensack Ave., Continental Plaza, 4th  
 : CITY: Hackensack  
 : STATE: New Jersey  
 : ZIP: 07601  
 : COMPUTER: IBM PC compatible  
 : SOFTWARE: IBM PC DOS/MS-DOS  
 : CURRENT APPLICATION DATA:  
 : FILING DATE: 08-SEP-1995  
 : PRIORITY APPLICATION NUMBER: US/08/906-865  
 : FILING DATE: 08-SEP-1995  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: JACKSON ESQ., DAVID A.  
 : TELEPHONE: (201) 243-1600  
 : TELEFAX: (201) 243-1600  
 : TELEPHONE: 201-243-1600  
 : INFORMATION FOR SEQ ID NO: 3:  
 : SEQUENCE CHARACTERISTICS:  
 : TYPE: amino acid  
 : STRANDNESS: single  
 : MOLECULE TYPE: protein  
 : DESCRIPTION: /desc = "Synapsin Ila"  
 : FRAGMENT TYPE: NO  
 : ORIGINAL SOURCE:

Query Match 5.2%; Score 94.5; DB 3; Length 582;  
 Best Local Similarity 22.8%; Pred. No. 0.34;  
 Matches 49; Conservative 20; Mismatches 85; Indels 61; Gaps 9;  
 Oy 6 INVEPLVTHQGPSPAPGAPGQGGTHTLSTPLATLVNWRAPPLGLPTSD 65  
 Db 26 LQEPPL--QGPFPFGCAASAAPTTAP-----GERPP--PASRAA 70  
 Oy 66 AQPPLVRLHQTTPSSHAGLSASRRRGRCATKCHGIRGWRRERNGAPAE 125  
 Db 71 GPAP-----TFVSQSFSSLSAVGTAAANLVD-----NPAP 105  
 Oy 126 APISVWRKPKWNSNGSTFLIMNCLIGQSGQVWITGLSSGKSTLACA 185

Db 106 ABAARAKAVLL--VYDFHAKNCFRG---KVLGDYDKVQAEFS-----149

Oy 186 LSEELJCRHLL--TVYLDQDRLHRLHLSFRAE 218

Db 150 ---ELNEVAHAGTAVDQVLRNGLKYNISFED 181

RESULT 14

US-08-815-718-2

Sequence 2: Application US/08815718

GENERAL INFORMATION:

APPLICANT: NI, JIAN

APPLICANT: DILLON, PATRICK

APPLICANT: GENTZ, REINER

NUMBER OF INVENTORS: 3

NUMBER OF INVENTORS: 3

INVENTORIAL DIFFERENTIATION FACTOR

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

COUNTRY: US

ZIP: 07069

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/815,718

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BISHOP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (201) 994-1700

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

TYPE: amino acids

TOPOLOGY: linear

MOLECULAR WEIGHT: protein

US-08-815-718-2

Query Match

Seq: 34; Db 2; Length 415;

Local Similarity 21.3%

Matches 64; Conservative 34; Mismatches 113; Indels 90; Gaps 15;

Oy 1 BRRIE-----INTEPVTHTQDPSAPASQDQNTLLEPPTLAVTL 48

Db 34 REHQVGAAPPSLSRLPH---DMPSQSGPPFQSQ---VPPFSQ--- 82

Oy 46 VNPQVAPVPLTSD---APLP---ALVHICPTPSSH---SSGLASDGRBG 95

Db 43 ATPLQKILQAPNAKEVGPVQAPVQLQKLSLQNMKQKATPFOQSNRP 142

Oy 97 RGRGATICH--RGIGVWYHRRNGAAGAPMSVKEKPSNIGK---STNLIH 149

Db 143 ESNNAKQKQDQSGW--GIRLQSPFG-----RPSDQALQCLNQAIVG 191

Oy 150 NCLIGDRLKQKQCVMTIGLSQSNKSLACLSRLKHCIRH---LTVYLDQ 204

Db 192 PMLFQSSYSLTRQ-----GUTFLVIGTSKICSTNHCLEKALWEY 240

Oy 205 LKMLGDLSTFADRAEMTRVGVKALFUNGVCIALSIPTFDKACHALPHSN 264

Db 241 LKXCDREYAVTHHH-----LCRRIPSPTRDCFARA--PTPN 279

Oy 265 F 265

Db 280 Y 280

RESULT 15

US-07-832-855-2

Sequence 2: Application US/07832855

GENERAL INFORMATION:

APPLICANT: LIA, Bernard

APPLICANT: LIA, Feiyong

TIME OF INVENTION: Methods and Compositions of a

NUMBER OF INVENTORS: 2

NUMBER OF INVENTORS: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOLLISTER & HUNTER

STREET: 321 No. 3478727th Clark Street, Suite 800

CITY: Chicago

STATE: Illinois

COUNTRY: US

ZIP: 60610

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/832,855

FILING DATE: 99/02/07

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Cooley, Ronald B.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 245-4900

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

TYPE: Amino acid

TOPOLOGY: linear

MOLECULAR WEIGHT: protein

US-07-832-855-2

Query Match

Seq: 91.5; Db 1; Length 635;

Local Similarity 33.0%

Matches 30; Conservative 7; Mismatches 43; Indels 11; Gaps 4;

Oy 6 INQTEPVTHTQDPSAPASQDQNTLLEPPTLAVTLVNRQAPVLP 60

Db 516 VTSIDAPALVYH---GLTPSSHISG 86

Oy 615 LGTSDAPALVYH---GLTPSSHISG 86

Db 576 -TUTALPTTPAPPTTSGSPFASINAG 605

Search completed: November 2, 2002, 01:54:10

Cost time : 22 secs





Qy 139 NIKSTNINWLNKLGDSKRLKQGVYVFTGLSSKSTLCAALSHCHGLTYL 198  
 Dd 2 NIKSTNINWLNKLGDSKRLKQGVYVFTGLSSKSTLCAALSHCHGLTYL 61  
 Qy 199 VLDGNIHRLGSLKADNENHVRVFAKLVADGVGCTASLSPFRDRCORA 258  
 Dd 62 LLDGNIHRLGSLKADNENHVRVFAKLVADGVGCTASLSPFRDRCORA 121  
 Qy 229 LPHFNSEVFTDLKTCAGDAPGKLVAKTQKIGTGIDDPYPPINSEVIT 315  
 Dd 132 LK-GKSTVAVTDCVSGVSGNGLNANZSLNLTGDSPPYPPINSEVIT 180  
 Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

## RESULT 5

A:Accession: A69839  
 C:Species: Bacillus halodurans

A:Residues: 1-199 <STD>  
 A:Reference number: A69839

A:Experimental source: strain 168  
 C:Superfamily: adenylylsulfate kinase

Query Match Similarity 30.4%; Score 555; DB 2; Length 199;  
 Matches 100; Conservative 27; Mismatches 44; Indels 0; Gaps 0;

Qy 145 NIKNMLGDSKRLKQGVYVFTGLSSKSTLCAALSHCHGLTYL 204  
 Dd 6 NIKNMLGDSKRLKQGVYVFTGLSSKSTLCAALSHCHGLTYL 60

Qy 205 LRLGNIHRLGSLKADNENHVRVFAKLVADGVGCTASLSPFRDRCORA 264  
 Dd 66 LRLGNIHRLGSLKADNENHVRVFAKLVADGVGCTASLSPFRDRCORA 126

Qy 265 FTDTVFDLTKTCAGDAPGKLVAKTQKIGTGIDDPYPPINSEVIT 315  
 Dd 136 FTDTVFDLTKTCAGDAPGKLVAKTQKIGTGIDDPYPPINSEVIT 176

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

C:Species: Bacillus halodurans  
 C:Accession: A69839  
 A:Residues: 1-204 <STD>  
 A:Reference number: A69839  
 A:Experimental source: strain C-125  
 C:Superfamily: adenylylsulfate kinase

Query Match Similarity 25.3%; Score 534.5; DB 2; Length 202;  
 Matches 106; Conservative 58; Mismatches 58; Indels 5; Gaps 2;

Qy 145 NIKNMLGDSKRLKQGVYVFTGLSSKSTLCAALSHCHGLTYL 204  
 Dd 6 NIKNMLGDSKRLKQGVYVFTGLSSKSTLCAALSHCHGLTYL 60

Qy 205 LRLGNIHRLGSLKADNENHVRVFAKLVADGVGCTASLSPFRDRCORA 264  
 Dd 66 LRLGNIHRLGSLKADNENHVRVFAKLVADGVGCTASLSPFRDRCORA 126

Qy 265 FTDTVFDLTKTCAGDAPGKLVAKTQKIGTGIDDPYPPINSEVIT 315  
 Dd 136 FTDTVFDLTKTCAGDAPGKLVAKTQKIGTGIDDPYPPINSEVIT 176

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
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 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200

Qy 316 MDKSPKAMAKVYCYLPELNTL 341  
 Dd 181 DTEKCK-----VNMTEYLAKHKL 200



















[illegible]

400	NIWLSGSLTIDRISNATVGG-----TLDGSHVRSNINWPDIDWVAARAKGTQY	411	NIWLSGSLTIDRISNATVGG-----TLDGSHVRSNINWPDIDWVAARAKGTQY
166	GYVNVITGLSSGSSATLCAASREHLCIGLITVLDGNEHGLHRLSPFADMDAINT	225	GYVNVITGLSSGSSATLCAASREHLCIGLITVLDGNEHGLHRLSPFADMDAINT
436	RVVATGLSSGSSATLVYDRJHAQRTFDLIDGNEHGLHRLSPFADMDAINT	511	RVVATGLSSGSSATLVYDRJHAQRTFDLIDGNEHGLHRLSPFADMDAINT
425	RIVGVALPAGAGATVCSALSYRNDKACALLPNSRIVETDLPKICEARPKGL	485	RIVGVALPAGAGATVCSALSYRNDKACALLPNSRIVETDLPKICEARPKGL
432	RVVATGLSSGSSATLVYDRJHAQRTFDLIDGNEHGLHRLSPFADMDAINT	511	RVVATGLSSGSSATLVYDRJHAQRTFDLIDGNEHGLHRLSPFADMDAINT
512	RIVATGLSSGSSATLVYDRJHAQRTFDLIDGNEHGLHRLSPFADMDAINT	571	RIVATGLSSGSSATLVYDRJHAQRTFDLIDGNEHGLHRLSPFADMDAINT
286	YKLAETKTKPTGTDITDPTPEPISGIVKKGDEICSPKAAKQVCTL	335	YKLAETKTKPTGTDITDPTPEPISGIVKKGDEICSPKAAKQVCTL
572	YANAGGLTIDPTDPTPEPISGIVKKGDEICSPKAAKQVCTL	618	YANAGGLTIDPTDPTPEPISGIVKKGDEICSPKAAKQVCTL
RESULT 9		RESULT 9	
NIDP_RHTR		NIDP_RHTR	
AC	05-07-1996 (rel. 34, Created)	AC	05-07-1996 (rel. 34, Created)
AD	01-07-1996 (rel. 34, Last sequence update)	AD	01-07-1996 (rel. 34, Last sequence update)
DT	16-OCT-2001 (rel. 40, Last annotation update)	DT	16-OCT-2001 (rel. 40, Last annotation update)
DE	Transferase (EC 2.7.7.41) [Sulfate adenylyltransferase]	DE	Transferase (EC 2.7.7.41) [Sulfate adenylyltransferase]
GN	adenylyltransferase	GN	adenylyltransferase
OX	NCBI-Taxid=398	OX	NCBI-Taxid=398
OC	Rhizobium tropici	OC	Rhizobium tropici
OC	Rhizobiaceae	OC	Rhizobiaceae
OC	Rhizobium	OC	Rhizobium
OC	Strain=CFN 299	OC	Strain=CFN 299
PC	STRAIN=CFN 299	PC	STRAIN=CFN 299
RE	Medline=9503535; PubMed=4975625	RE	Medline=9503535; PubMed=4975625
RT	Plantation and Characterization of Rhizobium tropical Mod factor	RT	Plantation and Characterization of Rhizobium tropical Mod factor
RU	Mod. Plant Microbe Interact. 9:492-500(1996).	RU	Mod. Plant Microbe Interact. 9:492-500(1996).
RU	[2]	RU	[2]
SC	SEQUENCE FROM N.A.	SC	SEQUENCE FROM N.A.
ST	STRAIN=CFN 299	ST	STRAIN=CFN 299
TX	Polch-Neloli J.L., Marroqui S., Souza C., Mayenli H., Lopez-Lara I.M.,	TX	Polch-Neloli J.L., Marroqui S., Souza C., Mayenli H., Lopez-Lara I.M.,
TX	Thomas-Oates J., Spaink H.P., Medias M.,	TX	Thomas-Oates J., Spaink H.P., Medias M.,
TX	Characterization of Rhizobium tropici C18V98 nodulation factors: The	TX	Characterization of Rhizobium tropici C18V98 nodulation factors: The
TX	Mod. Plant Microbe Interact. 9:151-163(1996)	TX	Mod. Plant Microbe Interact. 9:151-163(1996)
CC	FUNCTION: PROPOSED TO PROVIDE ACTIVATED SULFATE FOR 'TRANSFER TO	CC	FUNCTION: PROPOSED TO PROVIDE ACTIVATED SULFATE FOR 'TRANSFER TO
CC	NOD FACTOR. ATP SULFURASE MAY BE THE GPASIS, REGULATING ATP	CC	NOD FACTOR. ATP SULFURASE MAY BE THE GPASIS, REGULATING ATP
CC	FUNCTION: APS KINASE CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE	CC	FUNCTION: APS KINASE CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE
CC	(-3' BY SIMILARITY). ATP + sulfate -> phosphosulfate + adenylylsulfate	CC	(-3' BY SIMILARITY). ATP + sulfate -> phosphosulfate + adenylylsulfate
CC	CATALYTIC ACTIVITY: ATP + adenylylsulfate + ADP + 3'-	CC	CATALYTIC ACTIVITY: ATP + adenylylsulfate + ADP + 3'-
CC	phosphosulfate	CC	phosphosulfate
CC	PHYSICALLY ASSOCIATED	CC	PHYSICALLY ASSOCIATED
CC	SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE GTP-BINDING	CC	SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE GTP-BINDING
CC	ELEMENTARY FACTOR FAMILY, CYSD-NOD SUBFAMILY.	CC	ELEMENTARY FACTOR FAMILY, CYSD-NOD SUBFAMILY.
CC	SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO THE APS KINASE	CC	SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO THE APS KINASE
CC	FAMILY	CC	FAMILY
CC	SWISS-PROT: P18751	CC	SWISS-PROT: P18751
CC	Trinidad de Cienfuegos, Cuba	CC	Trinidad de Cienfuegos, Cuba
CC	European Bioinformatics Institute. There are no restrictions on	CC	European Bioinformatics Institute. There are no restrictions on
CC	use by non-profit institutions as long as its content and the	CC	use by non-profit institutions as long as its content and the
CC	software is properly acknowledged. For commercial organizations	CC	software is properly acknowledged. For commercial organizations
CC	enquiries require a license agreement (see <a href="http://www.ebi.ac.uk/Enquiry">http://www.ebi.ac.uk/Enquiry</a> )	CC	enquiries require a license agreement (see <a href="http://www.ebi.ac.uk/Enquiry">http://www.ebi.ac.uk/Enquiry</a> )











```

CC -1- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
CC -1- CATALYTIC ACTIVITY: ATP + adenylisulfate = ADP + 3'-
CC -1- CATALYTIC ACTIVITY: ATP + adenylylhistidine = ADP +
CC -1- PATHWAY: SECOND STEP IN THE SULFATE ASSIMILATION PATHWAY THAT
CC -1- LEADS TO THE BIOSYNTHESIS OF METHIONINE AND CYSTEINE.
CC -1- EC: 2.7.1.36
CC -----
CC This SWISS-PROT entry is copyrighted; it is produced through a collaboration
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CC or send an email to license@sib-sib.ch.
CC -----
CC PDB: Y08866; CAX70093.1;
DR InterPro: IPR002891; AMS_kinase.
DR Pfam: PF01503; AFS_Kinase.1.
DR SMART: SM00432; Afs_Kinase.1.
DR TrEMBL: F08866.1;
KW Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
KW Phosphorylation.
KW ACCT: 103 105 NTP (GENERAL).
KW ACT_SITE 103 105 KIMS THE PHOSPHOGERINE INTERMEDIATE (BY
KW SIMILARITY).
FT SEQUENCE 206 AA: 23028 MW: 54004832ZCALCD CRC64;
Query Match 26.6% Score 486; DB 1; Length 206;
Best Local Similarity 50.7%; Pred. No. 2e-29;
Matches 106; Conservative 30; Mismatches 61; Indels 12; Gaps 5;
QY 143 STNLIWNLGDSQKLGKQCVWITGLSGSKSTLACLSRELLCHGHULTYLDQ 202
DB 2 ATNIT-HAGLTWRNQLKNGLTINLTGLSASGSLTAVLEHQLQLGGLHATLQD 60
QY 203 NMLSEGNLSEFFAEERENRINVEVWAKPQAGKCTASISPRQDQACAL-L 260
DB 61 DNWVFLKALDGFSDGRNRIHIAVAKLPASSSIATFSFPADDDTARKLIEV 120
QY 261 PHSK-----PIETDLFLKCTARNGVGLYKARGIKGTGLQDPTPEINCEIVI 314
DB 121 PFMSTGGLPFVEVWVIEVAKRPGLYKARGIEIKETGTSSTPIAPENVEVH 180
QY 315 KMKDECTSFANAKVCLTLENGTLQA 343
DB 181 KND-LIQLQAV-LQIILGLSKLQDA 206

```

Search completed: November 2, 2002, 01:52:18  
Job time: 22 SECS













BA Unterbach T., Tran K., Wolf A., Vamsharan J., Ermolaeva M., White O.,  
 SA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.A., et al.  
 CC The complete genome sequence of *Caenorhabditis elegans*.  
 RL 1-1. SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 DR EMBL: C00892.2; AAC3461.1. -.  
 DR InterPro: IP002891; AFS.kinase.  
 DR IncePro: IP000795; GTP-BPTU. 1.  
 DR Pfam: PF01583; AFS.kinase. 1.  
 DR Pfam: PF00009; GTP-BPTU. 1.  
 DR Pfam: PF00019; GTP-BPTU. 1.  
 DR ProDom: PR002350; AFS.kinase. 1.  
 DR PRINTS: PR00315; ELONGATIONFCT.  
 KK Complete proteome: GTP-binding; Transferrase.  
 SO SEQUENCE 635 AA; 567FBH2AE653450 CRC64:  
 Query Match 27.8%; Score 508.5; DB 16; Length 635;  
 Best Local Similarity 51.3%; Pred. No. 1,4e-33;  
 Matches 100; Conservative 32; Mismatches 60; Indels 3; Gaps 1;  
 QY 142 KSTNLINMKLQGGKQKGVYWGVSSEKSTLACSLREHCGHLYTLD 201  
 DB 142 KSTNLINMKLQGGKQKGVYWGVSSEKSTLACSLREHCGHLYTLD 201  
 QY 436 RGNLHGLNDLSPFAEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 DB 436 RGNLHGLNDLSPFAEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 QY 496 GDNVHGLNDLSPFEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 DB 496 GDNVHGLNDLSPFEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 QY 262 HSNVFTVPLKAGDQVKGKLSKGLKGPQGLGVDSVHNPVYKRWYKMDRC 321  
 DB 262 HSNVFTVPLKAGDQVKGKLSKGLKGPQGLGVDSVHNPVYKRWYKMDRC 321  
 QY 556 PGFETVPTPLAARVDYGLTKKRSGLQNFYGVDSVPAESPELII--DTTA 612  
 DB 556 PGFETVPTPLAARVDYGLTKKRSGLQNFYGVDSVPAESPELII--DTTA 612  
 QY 322 PSPKANKVQCLTLE 336  
 DB 322 PSPKANKVQCLTLE 336  
 QY 613 ITPVDGKRVMLSE 627  
 DB 613 ITPVDGKRVMLSE 627  
 RESULT 11  
 QY 022501 PRELIMINARY; PRT: 652 AA.  
 AC 022501:1996 (T-EMBLrel. 01, Created)  
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
 DR EMBL: AB042791; P0761N.  
 CC Protein.  
 OS *Caenorhabditis elegans*.  
 CC *Caenorhabditis elegans*.  
 CC Rhabditidae: Rhabditidae.  
 CC Rhabditidae: Rhabditidae.  
 CC NCBI\_TaxID=6239;  
 CC SEQUENCE FROM N.A.  
 BA W1d. A1.  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 SO SEQUENCE FROM N.A.  
 QY MEDLINE=90069513; PubMed=985191;  
 RP MEDLINE=90069513; PubMed=985191;  
 RT 'Genome sequence of the nematode *C. elegans*: A platform for  
 RT investigating biology.';  
 RL 1-1. SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 DR EMBL: C00892.2; AAC3461.1. -.  
 DR InterPro: IP002891; AFS.kinase.  
 DR IncePro: IP000795; GTP-BPTU. 1.  
 DR Pfam: PF01583; AFS.kinase. 1.  
 DR Pfam: PF01747; ATP-sulfurylase. 1.  
 DR ProDom: PR002350; AFS.kinase. 1.  
 DR PRINTS: PR00315; ELONGATIONFCT. 1.  
 SO SEQUENCE 652 AA; 72887 MW; 36148F20C3A0875 CRC64:

Query Match 27.7%; Score 505.; DB 5; Length 652;  
 Best Local Similarity 48.0%; Pred. No. 2.8e-33;  
 Matches 100; Conservative 38; Mismatches 64; Indels 16; Gaps 6;  
 QY 125 EAPISPKYKPYNSNT--GASTNLINMKLQGGKQKGVYWGVSSEKSTLACSLREHCGHLYTLD 201  
 DB 125 EAPISPKYKPYNSNT--GASTNLINMKLQGGKQKGVYWGVSSEKSTLACSLREHCGHLYTLD 201  
 QY 10 BODMAPKAFYSSLSQGSNTTGTFTSREHAAAGVGHDFGCTITMFTVLSGAK 60  
 DB 10 BODMAPKAFYSSLSQGSNTTGTFTSREHAAAGVGHDFGCTITMFTVLSGAK 60  
 QY 180 STACSLASREHCGHLYTLDGNDHGLNDLSPFAEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 DB 180 STACSLASREHCGHLYTLDGNDHGLNDLSPFAEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 QY 239 TLTSTLELNLKLTGCTGLDNDHGLNDLSPFAEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 DB 239 TLTSTLELNLKLTGCTGLDNDHGLNDLSPFAEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 QY 240 TLTSTLELNLKLTGCTGLDNDHGLNDLSPFAEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 DB 240 TLTSTLELNLKLTGCTGLDNDHGLNDLSPFAEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 QY 130 ICALPTSPFEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 DB 130 ICALPTSPFEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 QY 298 TDTGTPPTPEKINSEKVM--ID--EEDPSKAMKQVLYSEKENTYL 341  
 DB 298 TDTGTPPTPEKINSEKVM--ID--EEDPSKAMKQVLYSEKENTYL 341  
 QY 190 TLTSTLELNLKLTGCTGLDNDHGLNDLSPFAEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 DB 190 TLTSTLELNLKLTGCTGLDNDHGLNDLSPFAEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 RESULT 12  
 QY 033856 PRELIMINARY; PRT: 627 AA.  
 AC 033856:2001 (T-EMBLrel. 19, Created)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
 DR EMBL: AB042791; P0761N.  
 CC Protein.  
 OS *Bradyrhizobium elkanii*.  
 CC *Bradyrhizobium elkanii*.  
 CC *Bradyrhizobium elkanii*.  
 CC NCBI\_TaxID=25448;  
 CC SEQUENCE FROM N.A.  
 BA STRAIN=USDA 94;  
 RL MEDLINE=153655; PubMed=167918;  
 RT 'DNA sequence and mutational analysis of rhizobiotin biosynthesis  
 RT genes in *Bradyrhizobium elkanii*.';  
 RL 1-1. SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 DR EMBL: AB042791; P0761N.  
 CC Protein.  
 QY SEQUENCE 627 AA; 68085 MW; 602N7489FC7978 CRC64:  
 Query Match 27.6%; Score 504.5; DB 2; Length 627;  
 Best Local Similarity 49.7%; Pred. No. 3e-33;  
 Matches 95; Conservative 34; Mismatches 59; Indels 3; Gaps 1;  
 QY 142 KSTNLINMKLQGGKQKGVYWGVSSEKSTLACSLREHCGHLYTLD 201  
 DB 142 KSTNLINMKLQGGKQKGVYWGVSSEKSTLACSLREHCGHLYTLD 201  
 QY 429 BAKHQAQVGRHRAEADLNGKGLTFTVLSGAKSGLNLTQVYLFKMSRANGLD 488  
 DB 429 BAKHQAQVGRHRAEADLNGKGLTFTVLSGAKSGLNLTQVYLFKMSRANGLD 488  
 QY 202 GINLRHGLNDLSPFAEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 DB 202 GINLRHGLNDLSPFAEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 QY 489 GDNVHGLNDLSPFEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 DB 489 GDNVHGLNDLSPFEDRAENIRVGVYKAFADGVCTISLSPFPRDRCALPL 261  
 QY 265 HSNVFTVPTPLAARVDYGLTKKRSGLQNFYGVDSVPAESPELII--DTTA 612  
 DB 265 HSNVFTVPTPLAARVDYGLTKKRSGLQNFYGVDSVPAESPELII--DTTA 612  
 QY 549 KKEEVEVFVDTPTPEKINSEKVM--ID--EEDPSKAMKQVLYSEKENTYL 341  
 DB 549 KKEEVEVFVDTPTPEKINSEKVM--ID--EEDPSKAMKQVLYSEKENTYL 341  
 QY 322 PSPKANKVQCLTLE 336  
 DB 322 PSPKANKVQCLTLE 336  
 QY 607 -TFQDQAVNT 616  
 DB 607 -TFQDQAVNT 616  
 RESULT 13  
 QY 09PT59 PRELIMINARY; PRT: 202 AA.  
 AC 09PT59:2000 (T-EMBLrel. 15, Created)  
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)

## ADENYLYLSULFATE KINASE.

DE Schizosaccharomyces pombe (Pisision yeast).  
 OS Bakerskaya, Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetes; Schizosaccharomycetes;  
 CC Schizosaccharomycetes;  
 OX NEB1\_TaxID=4896;

BP SEQUENCE FROM N.A.

SC STRAIN=972H;

RA Wood V., Rajandran M.A., Barrell B.G., Brown S., Harris D.;

DB EMBL: AL148036; CAB94733.1; GenBank/EMBL/GenBank/EMBL

DR InterPro: IPRO02891; AFS\_Kinase.

DE Problem: P000230; AFS\_Kinase; 1.

RM Kinase.

SK SEQUENCE 202 AA; 22669 MW; A5F7E4D53D7635B CRC64;

Query Match Similarity 27.6%; Score 503.5; DB 3; Length 202;

Matches 105; Conservative 7%; Penalties 84e-32; Indels 17; Gaps 4;

OY 143 STNLMNKLIGSGDKLQKGVYWTGLSSGKSTACALSELNCHGITYVLGG 202

DB 2 ATNIFPGSVTEERIFVGHQPTLMTGLSSGKSTACALSELNCHGITYVLGG 61

OY 203 DNLNGLNGLNGLSFKAKNIRNIRGVKAFADAGVICTASISFYPRDQACAL-- 259

DB 62 DNVGELGSLGSGDNRNIRGVKAFADAGVICTASISFYPRDQACALPHK 121

OY 260 --LPHSNITVDLPKICEADPKGLYKLTAKTKIGTIGTIDPTPEPPIKGTIV-- 315

DB 122 DGLP--LPHSNITVDLPKICEADPKGLYKLTAKTKIGTIGTIDPTPEPPIKGTIV-- 178

OY 316 -MKDEECPSPMAKAVQCYLIEE 337

DB 179 TQSTIEE-----VEKIVTLLR 195

RESULT 14

OSRYT1

AC OSRYT1

DR PRELIMINARY;

DT 01-MAR-2001 (TRENDEL, 16; Created)

DT 01-MAR-2001 (TRENDEL, 15; Last sequence update)

DT 01-MAR-2001 (TRENDEL, 37; Last annotation update)

DE AFS\_KINASE.

OS CS

DR Klebsiella aerogenes

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

CC Klebsiella

OX [1] --TaxID=88431.

BP SEQUENCE FROM N.A.

SC STRAIN=H70.

RA Seftian T.A., Lawrence J.C.;

DB EMBL: AF048468; AF048468.1; GenBank/EMBL/GenBank/EMBL

DR EMBL: AF048468; AF048468.1; GenBank/EMBL/GenBank/EMBL

DE Problem: P000230; AFS\_Kinase; 1.

RM Kinase.

SK SEQUENCE 201 AA; 22504 MW; 68B20A71AB03D712 CRC64;

Query Match

Best Local Similarity 27.5%; Score 493;

Matches 97; Conservative 27.7%; Penalties 9.1e-34;

OY 145 TMNKLNLIGSGDKLQKGVYWTGLSSGKSTACALSELNCHGITYVLGG 204

DB 145 TMNKLNLIGSGDKLQKGVYWTGLSSGKSTACALSELNCHGITYVLGG 66

OY 7 NYVHAUPTQOORHGHGIVLYLFTGLSSGKSTACALSELNCHGITYVLGG 66

DB 7 NYVHAUPTQOORHGHGIVLYLFTGLSSGKSTACALSELNCHGITYVLGG 66

OY 203 LARGELNGLSFKAKNIRNIRGVKAFADAGVICTASISFYPRDQACALPHSN 264

DB 203 LARGELNGLSFKAKNIRNIRGVKAFADAGVICTASISFYPRDQACALPHSN 264

OY 67 VLVGELGSLGSGDNRNIRGVKAFADAGVICTASISFYPRDQACALPHSN 126

DB 67 VLVGELGSLGSGDNRNIRGVKAFADAGVICTASISFYPRDQACALPHSN 126

OY 265 FIEVFDLPKICEADPKGLYKLTAKTKIGTIGTIDPTPEPPIKGTI 312

DB 265 FIEVFDLPKICEADPKGLYKLTAKTKIGTIGTIDPTPEPPIKGTI 312

OY 127 FIEVFDLPKICEADPKGLYKLTAKTKIGTIGTIDPTPEPPIKGTI 174

DB 127 FIEVFDLPKICEADPKGLYKLTAKTKIGTIGTIDPTPEPPIKGTI 174

RESULT 15

OSRYT1

AC OSRYT1

DR PRELIMINARY;

DT 02-DEC-98

DT 02-DEC-98

DE 01-NOV-1996 (TRENDEL, 01; Created)

DE 01-NOV-1996 (TRENDEL, 01; Last sequence update)

DE 01-NOV-2000 (TRENDEL, 37; Last annotation update)

DE PAPS SYNTHETASE.

OS Urethral caupo (inkkeeper worm) (Spoonworm)

OC Urethral caupo (inkkeeper worm) (Spoonworm)

OC NEB1\_TaxID=4431;

RM [1] SOURCE FROM N.A.

RA Rosenthal E., Leusath T.;

DB MEDLINE=9606529; PubMed=4522184;

DE ATP sulfiurylase and AFS kinase

RT ATP sulfiurylase and AFS kinase activities, 1;

RL Gene 165,243-246(1995);

DR InterPro: IPR002890; AFS\_Kinase.

DR InterPro: IPR002890; AFS\_Kinase.

DR PAPS SYNTHETASE; AFS\_Kinase; 1.

DR PAPS SYNTHETASE; AFS\_Kinase; 1.

DR Problem: P000230; AFS\_Kinase; 1.

DE Problem: P000230; AFS\_Kinase; 1.

SK SEQUENCE 817 AA; 88755 MW; 607C61B53AF2P70 CRC64;

Query Match

Best Local Similarity 20.3%; Score 502.5; DB 5; Length 610;

Matches 103; Conservative 34; Mismatches 31; Indels 21; Gaps 5;

OY 143 STNLMNKLIGSGDKLQKGVYWTGLSSGKSTACALSELNCHGITYVL 194

DB 10 ATNIFPGSVTEERIFVGHQPTLMTGLSSGKSTACALSELNCHGITYVL 69

OY 159 VLVGELNGLSFKAKNIRNIRGVKAFADAGVICTASISFYPRDQACAL 238

DB 159 VLVGELNGLSFKAKNIRNIRGVKAFADAGVICTASISFYPRDQACAL 238

OY 70 SLGDELNGLSFKAKNIRNIRGVKAFADAGVICTASISFYPRDQACAL 129

DB 70 SLGDELNGLSFKAKNIRNIRGVKAFADAGVICTASISFYPRDQACAL 129

OY 255 L--LPHSNITVDLPKICEADPKGLYKLTAKTKIGTIGTIDPTPEPPIKGTI 313

DB 255 L--LPHSNITVDLPKICEADPKGLYKLTAKTKIGTIGTIDPTPEPPIKGTI 313

OY 130 LARGELNGLSFKAKNIRNIRGVKAFADAGVICTASISFYPRDQACAL 166

DB 130 LARGELNGLSFKAKNIRNIRGVKAFADAGVICTASISFYPRDQACAL 166

OY 314 I---MKDEECPSPMAKAVQCYLIEE 339

DB 187 LTKAGNSIDE-----VOEVSYLEE 308

Search completed: November 2, 2002, 01:33:38

Job time : 68 secs

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2a model

Run on: November 2, 2002, 01:52:23 Search time 2245 Seconds  
3191.353 Million cell updates/sec

Title: US-09-720-384a-4

Perfect score: 1826

Sequence: 1 RFFHQTQELVTHQDP.....PRAMAVQVLYLENGVQA 343

Scoring table:

BLOSUM62  
Xaaop 10.0, Xaaext 0.5  
Xaaop 10.0, Yaaext 7.5  
Yaaop 10.0, Xaaext 7.5  
Delop 6.0, Delext 7.0

Searched: 1797656 seqs, 10463288293 residues

Total number of hits satisfying chosen parameters: 3595112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Command line parameters:

-MOEuf-frame\_p2a\_model -dbwexlin  
-db-GenBank1 -OMV-fastap -SUFFIX-frag -MINMATCH=0.1 -LOOPCL=0.1 -LOOPEX=0  
-UNIT8-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-huand40.cdi -LIST=45  
-OUTDIR-pro -NORMALIZE-HASIZE=300 -MINLEN=2000000000 -MODE-LOCAL  
-USBR-us09720384.rcn.1\_1773-fruqa\_1010202\_00537.19181 -NCPU=6 -ICPU=3  
-NBA1-TMPDIR=/tmp/ncba1 -NBA2-TMPDIR=/tmp/ncba2 -NBA3-TMPDIR=/tmp/ncba3  
-NBA4-TMPDIR=/tmp/ncba4 -NBA5-TMPDIR=/tmp/ncba5 -NBA6-TMPDIR=/tmp/ncba6  
-YAAOP=10 -YAAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Genbank: 1: gb-ba: \*  
2: gb-jtg: \*  
3: gb-jgi: \*  
4: gb-om: \*  
5: gb-ov: \*  
6: gb-oc: \*  
7: gb-ph: \*  
8: gb-pl: \*  
9: gb-pi: \*  
10: gb-pt: \*  
11: gb-st: \*  
12: gb-sy: \*  
13: gb-ty: \*  
14: gb-vi: \*  
15: gb-da: \*  
16: gb-hu: \*  
17: gb-in: \*  
18: gb-in: \*  
19: gb-in: \*  
20: gb-in: \*  
21: gb-in: \*  
22: gb-ov: \*  
23: gb-ov: \*  
24: gb-ph: \*  
25: gb-ph: \*  
26: gb-ro: \*  
27: gb-ro: \*  
28: gb-un: \*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
2	813	45.6	1086	8 AF044285	AF044285 Citabactam
3	816	44.7	1077	8 AF054238	U05238 Arbidol
4	816	44.7	1143	8 AF054287	AF054287 Arbidol
5	813.5	44.7	970	8 AF178976	AF178976 sea mays
6	778.5	42.6	1243	8 AF462823	AF462823 Arbidol
7	778.5	42.6	1243	8 AF462823	AF462823 Arbidol
8	633.5	34.7	3489	8 AF059759	AF059759 Arbidol
9	633.5	34.7	3489	8 AF059759	AF059759 Arbidol
10	633.5	34.7	3489	8 AF059759	AF059759 Arbidol
11	633.5	34.7	3489	8 AF059759	AF059759 Arbidol
12	633.5	34.7	3489	8 AF059759	AF059759 Arbidol
13	585.5	31.0	5353	1 B8T09476	B8T09476 B-subtilis
14	585.5	31.0	5353	1 B8T09476	B8T09476 B-subtilis
15	577	31.6	11131	1 AE075253	AE075253 Clostridi
16	563	30.8	2278	1 AM01682	AM01682 Clostridi
17	552	30.2	54330	2 AC104439	AC104439 Cyta sat
18	552	30.2	54330	2 AC104439	AC104439 Cyta sat
19	552	30.2	54330	2 AC104439	AC104439 Cyta sat
20	552	30.2	54330	2 AC104439	AC104439 Cyta sat
21	552	30.2	54330	2 AC104439	AC104439 Cyta sat
22	552	30.2	54330	2 AC104439	AC104439 Cyta sat
23	513	28.4	5386	1 AF084408	AF084408 Hbsaell
24	513	28.4	5386	1 AF084408	AF084408 Hbsaell
25	514	28.1	28401	1 AF062279	AF062279 Bradythiz
26	513	28.1	977	8 EC035193	EC035193 Penicillium
27	509.5	27.9	4042	1 FM4272	FM4272 Penicillium
28	509.5	27.9	4042	1 FM4272	FM4272 Penicillium
29	509.5	27.9	6013	1 RMO0890Q	RMO0890Q Rhizobium
30	509.5	27.9	6013	1 RMO0890Q	RMO0890Q Rhizobium
31	503	27.5	4037	1 RMO0890Q	RMO0890Q Rhizobium
32	503	27.5	4188	1 AE072737	AE072737 Sinorhizo
33	503	27.5	4188	1 AE072737	AE072737 Sinorhizo
34	502.5	27.5	2819	1 HU08AS01	HU08AS01 Sinorhizo
35	500.5	27.4	3561	1 AE080047	AE080047 Acetivirill
36	498.5	27.3	2141	10 AF004875	AF004875 Cavit por
37	498.5	27.3	2141	10 AF004875	AF004875 Cavit por
38	497.5	27.2	10580	1 AE036609	AE036609 Hmoella
39	496	27.2	2014	9 AF091242	AF091242 Hmo sapi
40	496	27.2	2014	9 AF091242	AF091242 Hmo sapi
41	496	27.2	2479	10 MG034883	MG034883 Mus muscu
42	496	27.2	2506	6 AF044160	AF044160 Mus muscu
43	496	27.2	2506	6 AF044160	AF044160 Mus muscu
44	496	27.2	3480	10 AF232758	AF232758 Cap sap
45	495	27.1	1875	6 E27970	E27970 Cap kinase

# ALIGNMENTS

RESULTS: 1  
LOCUS: AF044285  
DEFINITION: Citrananthus roseus adenosine-5'-phosphosulfate kinase (Crank)  
FEATURES: 1086 bp mRNA  
ACCESSION: AF044285  
VERSION: AF044285.1 GI:2812299  
SOURCE: Madagascar periwinkle.



















[illegible]





















[illegible]







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OM protein - nucleic search, using frame\_plus2n model

Run on: November 2, 2002, 01:54:13; Search time 197 seconds  
2889.348 Million cell updates/sec

Title: US-09-720-384a-4

Perfected score: 1926  
Sequence: 1 REFNNFNTPIVTTQFP...PKANAKOVLYLENNQLA 343

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Delgap 6.0, Delxext 7.0

Searched: 1736436 seqs, 45457221 res/diags

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0A

Maximum Match 100A

Listing first 45 summaries

Command line parameters:

-Q/cn1/USPTO/US09720384/frames\_30102020\_090227\_09173/APP-query.fasta\_1.519  
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24: /SIDSI/acidata/geneseq/geneseq-emb1/NA2002.DAT;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Length	DB	ID	Description
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2	876	48.0	928	21	AA250163	Maize Adenylisulph
3	876	48.0	928	21	AA250163	Maize Adenylisulph
4	852	46.7	936	21	AA250162	Soybean Adenylisulph
5	834	45.7	927	21	AA250164	Arabidopsis thalia
6	816	44.7	1068	21	AA250168	Arabidopsis thalia
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8	808	44.7	1193	21	AA250165	Arabidopsis thalia
9	778.5	42.6	917	21	AA250137	A. thaliana gene 1
10	778.5	42.6	917	21	AA250137	A. thaliana gene 1
11	778.5	42.6	948	21	AA250234	Arabidopsis thalia
12	752.3	41.5	1133	21	AA250161	Arabidopsis thalia
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16	486.5	26.6	2590	21	AA250166	Human DNA sequence
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18	455	27.1	1375	20	AA250167	Human DNA sequence
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25	481	26.3	606	22	AAH14465	Aspergillus oryzae
26	481	26.3	606	22	AAH14465	Aspergillus oryzae
27	454.5	24.9	868	31	AA250168	Human DNA sequence
28	419	22.9	588	21	AA250163	Maize Adenylisulph
29	330	18.3	347	22	AAH1282	Escherichia coli n
30	330	18.3	347	22	AAH1282	Escherichia coli n
31	314.5	17.2	34980	22	AAH1225	Proteobacter abysci
32	275.5	16.3	3342	21	AA250164	Maize Adenylisulph
33	275.5	16.3	3342	21	AA250164	Maize Adenylisulph
34	249	13.6	521	21	AA250164	Maize Adenylisulph
35	202.5	11.1	195	22	AAH17736	Human DNA sequence
36	202.5	11.1	195	22	AAH17736	Human DNA sequence
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38	202.5	11.1	195	22	AAH17736	Human DNA sequence
39	202.5	11.1	195	22	AAH17736	Human DNA sequence
40	189	10.4	471	22	AAH29209	Human foetal liver
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45	184	10.1	53500	21	AA255842	Complete nucleotide

## ALIGNMENTS

RESULT 1

AA250160

ID AA250160 standard; cDNA, 1217 bp.

AC AA250160;

XX 04-MAY-2000 (first entry)

XX

DE Corn Adenylisulphate kinase-2 cDNA clone

XX Adenylisulphate kinase; adenosine-5'-phosphatase kinase; APS kinase

XX 3'-Phospho-adenosine-5'-phosphatase; PAPS; sulphate assimilation;

KW corn; cDNA p0016.ctc1407b; transgenic plant; screen; antibody; ss.

OS

XX

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Oy 146 IIdenTtPhIsaGcRueAlIedIyGIsaRasptRGdIyIsaLauIdIyIs 165
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Oy 400 GCGTGTGTATGATGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACG 459
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XX 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 43768.
XX Hybridization assay: genomic overlap, gene expression control;
XX protein identification: signal transduction pathway;
XX metabolic pathway: promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX EF013040-A2.
XX 06-SEP-2000.
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Job time : 201 secs





GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: November 2, 2002, 01:57:13 ; Search time 16 seconds  
1831.372 Million cell updates/sec

Title: US-09-720-384a-4  
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Searched: 383333 seqs, 123816732 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB-Isued Patents WA -QNT-fastap -SUFFI-rml -MINMATCH=0.1 -ELOC=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -FRANS=human4.cdd  
-MODE=LOCAL -OUTFMT=ptc -NORWEST -HAPSIZE=300 -MINLEN=100 -ALIGN=0  
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-WARK-TIMEOUT=10 -FRESHSTART=0 -SCORES=0 -WAL=1 -LANG=0 -DBP-TIMEOUT=120  
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Database :

Issued Patents WA+  
1: /cgn2\_6/prodata2/1/a/SA\_COMB.seq\*  
2: /cgn2\_6/prodata2/1/a/SA\_COMB.seq\*  
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5: /cgn2\_6/prodata2/1/a/FCVUS\_COMB.seq\*  
6: /cgn2\_6/prodata2/1/a/backfiles.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	436	37.2	1500	US-08-371-551-4	Sequence 1, Appli
2	475	26.0	1160	US-09-151-310-41	Sequence 41, Appli
3	155	8.5	6803	US-08-665-259-19	Sequence 19, Appli
4	123	6.8	3329	US-08-144-000-19	Sequence 19, Appli
5	123	6.7	36741	US-09-301-665-3	Sequence 3, Appli
6	120.5	6.6	2377	US-09-461-474-5	Sequence 5, Appli
7	120.5	6.6	2626	US-08-156-020-5	Sequence 5, Appli
8	120.5	6.6	2626	US-08-156-020-7	Sequence 7, Appli
9	119.5	6.5	36319	US-08-423-137-2	Sequence 9, Appli

c 13	119	6.5	2499	3	US-07-502-848E-1	Sequence 1, Appli
c 15	117	6.4	1647	1	US-08-241-396-9	Sequence 9, Appli
c 16	117	6.4	1647	1	US-08-048-043-9	Sequence 9, Appli
c 17	117	6.4	1647	2	US-08-481-238-9	Sequence 9, Appli
c 18	117	6.4	1647	2	US-08-484-956-9	Sequence 9, Appli
c 19	117	6.4	1647	2	US-08-256-631-9	Sequence 9, Appli
c 20	117	6.4	1647	2	US-08-256-386-9	Sequence 9, Appli
c 21	117	6.4	1647	2	US-08-525-516-9	Sequence 9, Appli
c 22	117	6.4	1647	2	US-08-256-386-9	Sequence 9, Appli
c 23	117	6.4	1647	2	US-08-525-516-9	Sequence 9, Appli
c 24	117	6.4	1647	2	US-08-256-386-9	Sequence 9, Appli
c 25	117	6.4	1647	2	US-08-525-516-9	Sequence 9, Appli
c 26	117	6.4	1647	2	US-08-256-386-9	Sequence 9, Appli
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c 29	117	6.4	1647	2	US-08-525-516-9	Sequence 9, Appli
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c 31	117	6.4	1647	2	US-08-525-516-9	Sequence 9, Appli
c 32	117	6.4	1647	2	US-08-256-386-9	Sequence 9, Appli
c 33	117	6.4	1647	2	US-08-525-516-9	Sequence 9, Appli
c 34	117	6.4	1647	2	US-08-256-386-9	Sequence 9, Appli
c 35	117	6.4	1647	2	US-08-525-516-9	Sequence 9, Appli
c 36	117	6.4	1647	2	US-08-256-386-9	Sequence 9, Appli
c 37	117	6.4	1647	2	US-08-525-516-9	Sequence 9, Appli
c 38	117	6.4	1647	2	US-08-256-386-9	Sequence 9, Appli
c 39	117	6.4	1647	2	US-08-525-516-9	Sequence 9, Appli
c 40	117	6.4	1647	2	US-08-256-386-9	Sequence 9, Appli
c 41	117	6.4	1647	2	US-08-525-516-9	Sequence 9, Appli
c 42	117	6.4	1647	2	US-08-256-386-9	Sequence 9, Appli
c 43	117	6.4	1647	2	US-08-525-516-9	Sequence 9, Appli
c 44	117	6.4	1647	2	US-08-256-386-9	Sequence 9, Appli
c 45	117	6.4	1647	2	US-08-525-516-9	Sequence 9, Appli

## ALIGNMENTS

RESULTS 1 76-561-4  
? Sequence 4, Application US/0879561  
? Patent No. 5817482  
? GENERAL INFORMATION  
? APPLICANT: Hillman, Olan  
? APPLICANT: Hawkins, Jennifer L.  
? APPLICANT: Hillman, Olan  
? APPLICANT: Corley, Neil C.  
? TITLE OF INVENTOR: DISEASE RELATED NUCLEOTIDE KINASES  
? INVENTOR ADDRESS: 12  
? CORRESPONDENCE ADDRESS: 12  
? ADDRESSEE: Incyte Pharmaceuticals, Inc.  
? STREET: 3174 Porter Drive  
? STATE: CA  
? COUNTRY: USA  
? COMPUTER READABLE FORM:  
? MEDIUM TYPE: Diskette  
? SOFTWARE: FastSeq for Windows Version 2.0  
? CURRENT APPLICATION DATA: 08/879,561  
? FILING DATE: Herewith  
? CLASSIFICATION: 424  
? PUBLICATION DATA:  
? APPLICATION NUMBER:  
? FILING DATE:  
? ATTORNEY/AGENT INFORMATION:  
? REGISTRATION NUMBER: 1 36,749  
? REFERENCE/DOCKET NUMBER: PF-0325 US  
? TELECOMMUNICATION INFORMATION:

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? TELEPHONE: 415-855-0555
? TELEFAX: 415-845-4166
?
? INVOKED FOR SEQ ID NO. 4:
? SEQUENCE CHARACTERISTICS:
?   LENGTH: 2506 base pairs
?   TYPE: Linear
?   STRANDEDNESS: single
?   TOPOLOGY: linear
?
? IMMEDIATE SOURCE INFORMATION:
?   CLONE: pUC19
?   CLONE: 373887
?
? US-08-879-561-4
?
? Alignment Scores:
? Pred. No.: 2,186-33
? Score: 40.930
? Best Local Similarity: 45.42%
? Mismatches: 60
? Query Match: 34
? DB: 1
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? US-09-720-384A-4 (1-343) x US-08-879-561-4 (1-2506)
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? Oy 123 ProCluYeu1ProIsarProValuYeu1CluYeuPro-----135
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? Oy 9 CCGCGCTCTCAGCGCGCTCCGGCTGAGTATCGGAGACCTGTCGACGAGATC 68
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? Oy 136 ValMetSerAsh-----116GlySerThrAsnIleLeuTrpIle 149
?   ||||| ||||| ||||| ||||| |||||
? Oy 69 AGGTGAGTATACCGCGAGATCGGAGTACGACGACGACGATGATCAGCA 128
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? Oy 150 AAmCYeu1IleGlyuSerAspArgIuLeuLeuGlycin-----Lys 165
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? Oy 129 GCGCATATGTCAGCAGACAGCAGCAGTCTGTGGACGACGAGGTGGTTCT 188
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? Oy 166 GYCYuValuTrpIleTrpIleGlyuSerGlyuSerThrIleuAlaCYala 185
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? Oy 189 GGTTCACAGTGTGCTACAGCTCTGTGAGCGGAGAGACTACTGTGACATG 248
?   ||||| ||||| ||||| ||||| |||||
? Oy 186 LeuSerArgIuLeuIleuCYuSerGlyuSerIleuTrpIleuLeuSer 205
?   ||||| ||||| ||||| ||||| |||||
? Oy 249 TTGAGGAGTACTGTTTGTCTATGATATCTGTCAGCTCTGATGTGACAT 308
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? Oy 206 ArgIleuGlyuSerAspLeuSerPhyLysAlaGluLysArgIleuLeu 225
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? Oy 369 CCGATCCGAGGTCTTCACTCTTGTGATGCTGTGATGCTGTATGTCAC 428
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?
? RESULT 2

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US-09-153-310-41
? Sequence 41, Application US/0915310
? Patent No. 6326184
? General Information:
? APPLICANT: Gjermansen, Claes
? Inventor: Hansen, Jorgen
? Address: 1000 K Street, N.W.
? City: Washington
? State: DC
? Country: USA
? Inventor Address: 1000 K Street, N.W.
? City: Washington
? State: DC
? Country: USA
? Title of Invention: Method of producing a composite
? material and storage using genetically modified yeast
? strains
?
? NUMBER OF SOURCES: 42
? COMPARISON METHOD: BLAST
? ADDRESSES: Foley & Lardner
? 3500 K Street, N.W.
? Washington
? STATE: DC
? COUNTRY: USA
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? SOFTWARE: PARSISO for Windows Version 2.0
? CURRENT APPLICATION DATA: US/09/153, 310
? PENDING APPLICATION NUMBER: 09/153,310
? FILING DATE: 15-SEP-1998
? CLASSIFICATION: <unknown>
? PRIOR APPLICATION NUMBER: <unknown>
? FILING DATE: <unknown>
? ATTORNEY/AGENT INFORMATION:
? REGISTRATION NUMBER: 23,768
? REFERENCE/DOCKET NUMBER: <unknown>
? TELEPHONE: 202-672-5300
? TELEFAX: 202-672-5399
? INFORMATION FOR SEQ ID NO. 41:
? SEQUENCE CHARACTERISTICS:
?   LENGTH: 1160 base pairs
?   TYPE: Linear
?   STRANDEDNESS: single
?   TOPOLOGY: linear
?   MOL. WEIGHT: 386.00 kDa
?   SEQUENCE DESCRIPTION: SEQ ID NO: 41:
?
? US-09-153-310-41
? Alignment Scores:
? Pred. No.: 4,476-32
? Score: 475.00
? Best Local Similarity: 53.80%
? Mismatches: 26.01%
? Query Match: 6
? DB: 4
?
? US-09-720-384A-4 (1-343) x US-09-153-310-41 (1-1160)
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? Oy 163 GlyGlyuGlyuValuValuTrpIleuTrpIleuGlyuSerGlyuSerThrIleu 182
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? Oy 438 AAmCYeu1IleGlyuSerGlyuSerGlyuSerGlyuSerGlyuSer 497
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Oy 187 ratgclgdu 190
Db 24665 GCCTGAGTTG 2674
BS-09-461-474-5
: Sequence 5, Application US/09461474
: Patent No. 6278042
: APPLICANT: Alton, Steve
: APPLICANT: Rafelski, Antoni
: TITLE OF INVENTION: Metal Transporters
: FILE REFERENCE: 881303 US NA
: CURRENT APPLICATION NUMBER: US/09461474
: EARLIER APPLICATION NUMBER: 60/112,562
: EARLIER FILING DATE: 1998-12-16
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 5
: SEQ ID NO 1377
: TYPE: DN
: ORGANISM: Triticum aestivum
US-09-461-474-5
Alignment Scores:
Pred. No.: 0,206
Matches: 18
Percent Similarity: 30,53%
Best Local Similarity: 23,00%
Mismatches: 125
Indels: 171
Query Match: 4
Gaps: 22
US-09-720-384a-4 (1-343) x US-09-461-474-5 (1-1377)
Oy 4 HsPheLIeAnGlnTclGpLeuValHsThrGlnProSerPro--- 22
Db 139 CATTTCGCCCAAAATGCTCCGCTGCTTTCTCCCGGAGATGCTTCGACCTCTC 196
Oy 23 -----AlaPdcGlyProAlaSer-----GlnGlyGln- 31
Db 199 TACAGTCTCTCTGAGAGCCGAGCCTTGTGGATCTTGTGGCGGAGAGCGTG 258
Oy 32 -----ArgGlnGlyAnthrIle 38
Db 259 TGGCAGAGACGACCTTCTCTCTCTGCGATCTGAGTCAGCTCCAGCTCGCTG 318
Oy 38 user----- 38
Db 319 TTCTCTGCTCTCCAGCGATCCGCCCATACCTTCGATGCTCTCTCAGAGATTG 378
Oy 51 cdlGclgAlaPdpGpLeuPdcGlyLeuHsProSerApAlaPdcGlnProAla 71
Db 379 GZMAGAGCCGCTCTGACAGCTGGTTTGACACTGAG----- 418
Oy 71 wAlHsHsGlyLeuHsProGysSerHsSerAlaGlyLeuAlaSerApSe 91
Db 419 -----TCCGCTGAGAGCCGAGATGCGACACTTC-----GATATCTGTACAGCC 468
Oy 91 -GlyArg-----ArgGlnGlyGln 98
Db 469 AGGGAGGAGCCGATGAGTACAGCTTCGCGCTGTGCTCTGGAGAGCGATGAG 528
Oy 98 yNtGclGAlaTstHsLcYsHsIaTgGlyIleGlyAlaGtPwAlaGtAgTAg 118
Db 529 ATCTGGCATGCC-----AATCCCTGGTGTGAGAGCTATGT 567
Oy 118 gAndGlyAlaAlaPro-----GlyGlyAlaPro----- 128
Db 568 CTTTCGCGAGCTCTCAAGCAATCAATGCTCTCTCATAGAGACATCTCTCGACA 627

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Oy 128 sSerProValGclGlyProValHsSerAenIleGlySerThiAenIleLeuTr 148
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Oy 148 pHisAAsCysLeuIleGlyGln-SerAerGlnYsLeuLeuGlyGlnYsGlyCysV 168
Db 668 -CAGCTCTCTGAGAGCCTCTCCGCAAGGTTCTCACTCTGCTGCGACATATGTGCTC 726
Oy 168 alValTtPleHtGlyLeuSerGlyLeuSerGlySerThiLeuAlaCysAlaLeuSerA 188
Db 727 TC-----CTCAAGCTTCTGCTGCTGCGAG----- 752
Oy 188 tGdLeuHsIleCysArgGlySerThiTyValLeuAspGlyAspAsnLeuHsIle 208
Db 753 -----GTCNACTAGCC-----ACGACAGACAGCTC----- 779
Oy 208 tYLeuAsnAlaPdpGpLeuSerPheHisGlyAlaGlyAlaPdpGpLeuIleArgYsV 228
Db 822 -----AATGATGATCTCAGACATCTGAATCTCTCCGAGAGCCTC----- 822
Oy 228 tYGLValAlaYsLeuPheAlaAspAlaGlyVal-----tYcYsAlaIle 243
Db 823 CGAGGCTCAATCTCACTTGGACCTCGACCTCACTCACTTGTCTGTGTGCTGATTG 882
Oy 243 tAsErLeuIleSerProTyAsTAsTAsPAsTAs----- 253
Db 884 CAGATCTTCAAGTCTCTCGAGAGCGGCGTGTGATCAGAGCTTCTGCTGTATGTGTA 942
Oy 254 ----- 254
Db 943 TCAATCCACTCTAGCTGTGTCAACCACTCTCTCTCCCGAGAGCCTACGATTCG 1002
Oy 1003 ATCACTGACAGCCGCTCGACAGATCGAGAGCAGTATCTTGACAGTATGAGAGCAT 1062
Oy 265 tAlIleGlyLysPhe-----tLeuAspLeuProGlyLeuGlyAlaIleArgAspPro 283
Db 1063 ATCTGAGAGCTCTCAATGCTCTCAGATGCTCTCTCTTGAGAGCTACAGAGAG 1122
Oy 283 ySGLYLeuTyYsLeuAlaArgGlyGlyYsIleYsGlyPheHsGlytLeuAspP 303
Db 1123 AGAGCTCTGAGAGTTTACTGAATG-----CTGTGTACAC 1158
Oy 303 rGfyGlyUpPro-----tLeuAsnGlyGlyIleVal 314
Db 1159 CTTATGTTCTCTCTGATGAGGCTGTATCAGGCTAGCATAGAGCTGATGTGAT 1218
Oy 314 telysMeLyAsp 318
Db 1219 ATGAGAGAGCGAT 1232
RESULT 8
: Sequence 3, Application US/08156020
: Patent No. 5474920
: APPLICANT INFORMATION:
: APPLICANT: M. D., Bobb E.
: TITLE OF INVENTION: Modified Thermo-Resistant DNA
: TYPE OF INVENTION: Polymerases
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Allegrretti & Mitcoff
: STREET: 6500 South Wacker Drive
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: COUNTY: Cook
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: MEDIUM: 5.25 inch, 1.44 MB
: OPERATING SYSTEM: Macintosh
: SOFTWARE: Patentin Release #1.0, Version #1.25

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1  TITLE OF INVENTION: Polymerases
2  NUMBER OF SEQUENCE: 13
3  CORRESPONDENCE ADDRESS:
4  INVENTOR: Stephen A. Witcoff
5  STREET: 10 South Street Elite
6  CITY: Chicago
7  STATE: IL USA
8  ZIP: 60605
9
10 COMPUTER READABLE FORM:
11 FILE NAME: us09720384a.rn1
12 COMPUTER: Apple Macintosh
13 OPERATING SYSTEM: Macintosh
14 INVENTOR'S ATTORNEY: Patent in Release #1.0, Version #1.25
15 CURRENT APPLICATION NUMBER: US/08/156,020
16 FILING DATE: 04/13/00
17 NAME: Greenfield Ph.D., Michael S.
18 ADDRESS: 1327 N. Lincoln Ave.
19 REFERENCE/JOCKET NUMBER: 93, 413
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: (312) 715-1240
22 FAX: (312) 715-1240
23 INFORMATION FOR SEQ ID NO: 5:
24 SOURCE CHARACTERISTICS:
25 TYPE: nucleic acid
26 STRANDNESS: single
27 MOLECULE TYPE: DNA (genomic)
28 INFORMATION: NO
29 ORGANISM: Thermus aquaticus
30 ORIGINAL SOURCE:
31
32 FEATURE: mutation
33 LOCATION: replace(89, "g")
34 OTHER INFORMATION: /note="This mutation results in a nucleotide change from G to A. This results in an amino acid change of Phe to Ile."
35 OTHER INFORMATION: /note="This mutation results in a nucleotide change from G to A. This results in an amino acid change of Phe to Ile."
36
37 FEATURE: mutation
38 LOCATION: replace(934, "a")
39 OTHER INFORMATION: /note="This mutation results in a nucleotide change from G to A. This results in an amino acid change of Phe to Ile."
40 OTHER INFORMATION: /note="This mutation results in a nucleotide change from G to A. This results in an amino acid change of Phe to Ile."
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42 FEATURE: mutation
43 LOCATION: replace(962, "c")
44 OTHER INFORMATION: /note="This mutation results in a nucleotide change from G to A. This results in an amino acid change of Phe to Ile."
45 OTHER INFORMATION: /note="This mutation results in a nucleotide change from G to A. This results in an amino acid change of Phe to Ile."
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47 FEATURE: mutation
48 LOCATION: replace(2535, "a")
49 OTHER INFORMATION: /note="This mutation results in a nucleotide change from G to A. This results in an amino acid change of Phe to Ile."
50 OTHER INFORMATION: /note="This mutation results in a nucleotide change from G to A. This results in an amino acid change of Phe to Ile."
51
52 FEATURE: mutation
53 LOCATION: replace(193, "t")
54 OTHER INFORMATION: /note="This mutation results in a nucleotide change from G to A. This results in an amino acid change of Phe to Ile."
55 OTHER INFORMATION: /note="This mutation results in a nucleotide change from G to A. This results in an amino acid change of Phe to Ile."
56
57 FEATURE: mutation
58 LOCATION: replace(504, "a")
59 OTHER INFORMATION: /note="This mutation results in a nucleotide change from G to A. This results in an amino acid change of Phe to Ile."
60 OTHER INFORMATION: /note="This mutation results in a nucleotide change from G to A. This results in an amino acid change of Phe to Ile."
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Oy 118 -----KqAaScIyAlaAaProGlycUaA 126
Db 1210 CTTCCTCAAGGCGAGAGACTCGTTGGGAGAGAGCCCGCGCGCTTCCTCAGGT 1151
Oy 127 Pro-----HlSerProValyglLylProValMetSerAnIle 140
Db 1150 CDTGAGGCGCTTTAAGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1091
Oy 141 GlyySerThrAenIleuTrpHisAanCysIleuIleCylInSerAspGlnIly 160
Db 1090 GGCChAaAGATCGCCCAACAGCGCGCTTCCTGGGGAAGCGACCGACCGAGCGCC 1031
Oy 161 LeuIleuIyGlyIleCylIyValTrpIleThrGlyIyAuerSerIySerIy 180
Db 1030 CTTCCT-GCC-----GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCC 1005
Oy 181 ThrIleuIyCylAAsaSerIeSgdIleuHlscY-----AglIyIleuIleTrpVal 199
Db 1004 TCAAGGCGCTGGGCGCTTCGAGAGCGAGCGACTCGTGGAGGGG-----960
Oy 200 LeuAsgIyAspAenIleuArgHis-----Leu 213
Db 959 CTGCACACATCAAGCTCTCTCAGATAGGGCGCTTCCGCGCGCGCGCGCGCGCGCT 900
Oy 214 SerPheIyAlaLunAaPheAlaGluAenIleArgArgValCylValAlaIyLeu 233
Db 899 TTGGCGACATCCACTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Oy 234 PheAlaAspAlaCylIyAlleCylIleAlaSerLeuIleSerProArgArgAspArg 253
Db 839 TTGGATCTCTATGTGGCGCGCGCGCTCTCTCCGATGGCGCGCGCGCTTCACCGGTC 780
Oy 254 AspAlaAraAla---LeuLeuProHlSer-----AspPheIleIleValPheIle 270
Db 779 TTCTAGAGAGGCGCTCGAGGCTTCGCGCGCTTCGAGCGCTTCGCGCGCTTCCTCC 720
Oy 271 AspLeuProIleu 274
Db 719 CGATGCGCTTG 708
RESULT 11
US-08-156-020-9/C
Sequence 9, Application US/08156020
INVENTOR INFORMATION:
APPLICANT: Moses M.D., Robb E.
TITLE OF INVENTION: Modified Thermo-Resistant DNA
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
STREET: 10 South Nuclear Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
OPERATING SYSTEM: Macintosh
COMPUTER: Apple Macintosh
CURRENT APPLICATION DATA: Case #1.0, Version #1.25
APPLICATION NUMBER: US/08/156,020
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D. Michael S.
REFERENCE/DOCKET NUMBER: 93,413
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1214
TELEFAX:
INFORMATION FOR SEQ ID NO: 9:

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SEQUENCE CHARACTERISTICS:
LENGTH: 2626 base pairs
TYPE: nucleic acid
SOURCE: Human genome
MOLECULE TYPE: Linear
HYPOTHETICAL: NO
NAME/KEY: mutation
LOCATION: replace(89, "G")
OTHER INFORMATION: "this mutation results in a nucleotide alteration at position 89 of the native Tag DNA"
OTHER INFORMATION: polymerase nucleotide sequence of C to G.
NAME/KEY: mutation
LOCATION: replace(934, "A")
OTHER INFORMATION: "this mutation results in a nucleotide alteration at position 934 of the native Tag DNA"
OTHER INFORMATION: polymerase nucleotide sequence of T to A. This results in amino acid change of Phe to Ile.
NAME/KEY: mutation
LOCATION: replace(962, "C")
OTHER INFORMATION: "this mutation results in a nucleotide alteration at position 962 of the native Tag DNA"
OTHER INFORMATION: polymerase nucleotide sequence of T to C. This results in amino acid change of Leu to Pro.
NAME/KEY: mutation
LOCATION: replace(2335, "A")
OTHER INFORMATION: "this mutation results in a nucleotide alteration at position 2335 of the native Tag DNA"
OTHER INFORMATION: polymerase nucleotide sequence of G to A. This mutation is conservative.
NAME/KEY: mutation
LOCATION: replace(337, "G")
OTHER INFORMATION: "this mutation results in a nucleotide alteration at position 337 of the native Tag DNA"
OTHER INFORMATION: polymerase nucleotide sequence of A to G. This change results in an amino acid change of Phe to Leu.
NAME/KEY: CDS
FEATURE: CODON
FEATURE: LEU...2619
NAME/KEY: mat_peptide
FEATURE: LEU...2616
NAME/KEY: 1
FEATURE: LEU...2619
LOCATION INFORMATION: /note= "Prinf2"
US-08-156-020-9
Alignment Scores:
Prod. No. Length: 2626
Score: 120.50
Percent Similarity: 85
Identicality: 26.23
Similarity: 128
Query Match: 6.60%
Indels: 15
Gaps: 1
US-08-720-384A-4 (1-343) x US-08-156-020-9 (1-2626)
Oy 17 GluGluProPheSerProAlaProGlyProAlaSerGluGlyCysArgGluCylValThr 36
Db 1606 CAAGAAGACCGCTTCAGCT---GGTCCGGAGGTGTGAGTGTGAGGTGGCGGCCA 1350
Oy 37 LeuLeuSerThrProThrIleuValIleIleValIleValProIleArgIlePro 56
Db 1549 GCGCAAGACGACTCGCCT-----CGAGCGCGCGCGCGCGCGCGCGCGCGCG 1311
Oy 57 ValLeuProGlyLeuThrProSerAspAlaProLeuProAlaLeu-----71

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RESULT 15  
 US-08-254-359a-9 (1)  
 GENERAL INFORMATION: US-08-254-359a  
 Patent No. 5614402  
 APPLICANT: LYMICHEV, VICTOR I.  
 APPLICANT: BROW, MARY ANN D.  
 TITLE OF INVENTION: DNA POLYMERASE  
 NUMBER OF SEQUENCES: 40  
 CORRESPONDENCE ADDRESS:  
 STREET: 220 KONTOMERY STREET, SUITE 2200  
 CITY: SAN FRANCISCO  
 STATE: CALIFORNIA  
 COUNTRY: UNITED STATES OF AMERICA  
 ZIP: 94104  
 CONTACT PERSON: EUGENIE FLOPPY, sk  
 MEDIUM TYPE: DNA  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US-08-254-359a  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 PENDING NUMBER: US 08/073,384  
 FILING DATE: 05-JUN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/986,130  
 FILING DATE: 05-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CARROLL, PETER C.  
 REFERENCE/DOCKET NUMBER: POPS-01000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 397-8338  
 TELEFAX: (415) 397-8338  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1647 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 MOLECULE TYPE: DNA (genomic)  
 US-08-254-359a-9  
 Alignment Scores:  
 Pred. No.: 0,538 Length: 1647  
 Score: Similarity: 17,00  
 Match: 12,00  
 Best Local Similarity: 26,01% Mismatches: 21  
 Query Match: 6,41% Indels: 130  
 Gaps: 14  
 US-08-720-384a-4 (1-343) x US-08-254-359a-9 (1-1647)  
 Oy 37 GlnGlnProSerProLeuProGlyProLeuSerGlnGlyGlnGlyLeuThr 36  
 Db 1489 CAAGAGAGCCCTTCACCTCT---GGTCCGAGATGTGGGTGAGGGGTCCGCGCA 1433  
 Oy 37 LeuLeuSerProThrProThrProLeuAlaValLeuValLeuProGlnArgAlaPro 56  
 Db 1432 GCGCGAGAGCTTCGCTCT---CGAGCGGCGCATCTCCCGC 1394  
 Oy 57 ValLeuProGlyLeuThrProSerAspAlaProLeuProAlaLeu 71  
 Db 1393 CAGCTCCAGGAGCAAGGCGCTGAGTATGGCGCTGAGCGCACCCGCTGGCTCA 1334  
 Oy 72 -----ValIleIleGlyLeuThr 77

Db 1333 TGTGGCCAGCAGCGAGGAGGCGCTCTCACTCCGAGTAAGCAAGAGGCTCT 1274  
 Oy 78 ProAsySerSerIleSerSerAlaLy-----LeuLeuSerAspSerGlyArg----- 93  
 Db 1273 CTTCCCTCCCTCAAGCTCTCCCTCCCTCAAGCTCTCCGAGAGGCTCTCGAAGAGCGCCCT 1214  
 Oy 94 -----ArgGlyGlyGlyGlyArgGlyAlaArgThrIleCys 105  
 Db 1213 CCCCAGCTCTCTCCCTCCCTCTCCCTCCCTCCGCGCGGCGACCCCTCCGAGGTGGTGT 1154  
 Oy 106 HlaAsGlyLy-----IleIleArgThrValArgArgArg----- 117  
 Db 1153 TGGAGAGCTTCAGAGGTAGCGAGGAGCATGCGGCTGTCTCCGCGCGGAGCGCAGCG 1094  
 Oy 118 -----ArgAspGlyAlaProGlyGluLeu 126  
 Db 1093 CTTCCTCAAGGCGCAGAGCTCAGCTCTTGGCAGAGGCCCGCGCTCTTCAGST 1034  
 Oy 127 Pro-----HlaSerProValLyGlyLyArgProIleMetSerAspIle 140  
 Db 1033 CCTCAGGCTTTATAGCTCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 974  
 Oy 141 GlyLySerThrAsnIleLeuIlePheIleAlaCysLeuIleGlnSerAspArgGlnLy 160  
 Db 973 GGGCAGAGATGGCCACCATGGCTCTCTCGCGAAGAGCAAGGCCACAGAGCGC 914  
 Oy 161 LeuLeuGlyGlyLyGlyCysValValIleThrGlyLeuSerGlySerGlyLysSer 180  
 Db 913 CTCTCC-GC-----GGGGCGCAGAGGGCGCTCC 888  
 Oy 201 AspIleAspMetLeuThrGln-----GlyLeuAsnArgAsp-----LeuSer 214  
 Db 839 CCAATCTCAAGCTCTCCAGAGAGCGCTTACGCTCTCCGCTGGGCTCCGCTCTTGT 780  
 Oy 215 PheGlyAspGlnAspArgAlaValIleArgArgArgValGlyValAlaLyLeuPhe 234  
 Db 779 CCGAGATGACCTCCAGGCGCAGCTGCGCGACCTTGGCAGTCCCGAGAGAGCTTC 720  
 Oy 235 AlaAlaGlyValIleCysIleAlaSerLeuLeuLeuProThrArgArgAspArg 254  
 Db 719 AGATCTCCATCTGGCCAGAGCTCTCTCCGGATGGCGGCTCTACGCGCTCAAGTTC 660  
 Oy 255 AlaCysArgAla-----LeuLeuProIleHis-----AsnPheIleValPheIleAsp 271  
 Db 659 TTGAGAGAGCTTCCAGGCTCCGCGCTCTCTCAGAGAGAGCTCTTCGCGCTTTTCGCG 600  
 Oy 272 LeuProLeu 274  
 Db 599 ATGCTCTTG 591  
 Search completed: November 2, 2002, 01:10:12  
 Job Time 74 secs



















Baker, B  
 Generation of ESTs from in vitro grown microtubers  
 JOURNAL  
 CONTACT: Cathy Romling  
 The Institute for Genomic Research  
 9700 Rockville Pike  
 Division tel 1-800-711-6195, email cdm@regen.com  
 Seq primer: M1P-R.  
 1. Location/Qualifiers  
 FEATURES  
 SOURCE  
 /db\_xref="taxid:31413"  
 /clone\_lib="cSTF"  
 /cvs="axillary buds of stem explants; growing  
 sink tubers"  
 /dev\_stage="7, 8 and 10 days"  
 /organism="Solanum tuberosum"  
 /project="Biotic"  
 /submitter="Biotic"  
 /db\_xref="GeneID:1413"  
 /clone\_lib="cSTF15315"  
 /note="Vector: pBluescript SK(+); Site 1: Roob; Site 2:  
 XhoI; tissue supplied by Christian Buchen and Richard  
 Wenzel. The tubers were supplied by the Regeneron  
 unit. The tubers were grown in vitro. The tubers will  
 attempt to capture the induction and initiation/initial  
 growth of the tuber in an in vitro system as described in  
 the following paper: Romling, C. et al. (1999) "In vitro  
 development of axillary buds attached to stem explants when  
 placed on a high sucrose medium (10%)." Visible  
 development of axillary buds was observed after five in  
 vitro days. The first library, cSTF (1-20) consists  
 of axillary buds harvested on days 1-3. This targets  
 genes involved in tuber initiation and outgrowth. The  
 following libraries, cSTF (21-40) and cSTF (41-60),  
 capture genes involved in tuber initiation and outgrowth.  
 This library is noted as p3 in Tansley lab notebooks.  
 BASE COUNT 212 a 137 c 219 g 218 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 786  
 Score: 672.50  
 Similarity: 88.74%  
 Best Local Similarity: 76.67%  
 Query Match: 36.83%  
 Indels: 2  
 Gaps: 0

us-09-720-384a-4 (1-343) x BL178754 (1-786)  
 Oy 135 Prov1metSerAnGlyGlySerTherAnLeuTrpHisAcnGlyLeuTleCly 154  
 Db 278 CCTGAGTCTTCACATAGAGAGTATCAACAAACATCTGCGACACGCTGTGAG 337  
 Oy 155 GlnSerAspAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 174  
 Db 338 AATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 397  
 Oy 175 SerClySerClySerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 194  
 Db 348 ATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 457  
 Oy 195 HsAlaCysGlyAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 214  
 Db 458 AACCTACCTATATCTGATGATGATGATGATGATGATGATGATGATGATGAT 517  
 Oy 215 PheValAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 234  
 Db 518 TCCACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 577  
 Oy 235 AlaAlaPheAlaGlyValAlaLysCysValLysSerProPheValPheValPhe 254  
 Db 578 GGGATATCTGGAGCTATATCTGGAGCTATATCTGGAGCTATATCTGGAGCA 637  
 Oy 255 AlaCysGAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 274

Db 638 GCTGCTGCTGCTTACTCTACGAGAGGATCTTACGAGGATCTTACGAGGATCTT 697  
 Oy 275 TysLeuGlyGlyAlaAspProGlySerGlyLeuGlyAlaGlyGlyGlyGlyGly 294  
 Db 698 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 756  
 Oy 295 TysGlyPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 304  
 Db 757 AACT-TTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 784  
 RESUME 12  
 LOCUS A1637166/c 602 bp mRNA linear EST 26-APR-1999  
 DEFINITION A1637166.X1.003 - stressed root cDNA library from Wang/Bohnert lab  
 A1637166.cDNA, mRNA sequence.  
 VERSION A1637166.1 GI:4688496  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 REFERENCE  
 TITLE Male ESTs from various cDNA libraries sequenced at Stanford  
 COMMENT  
 CONTACT: Walbot V  
 Department of Biological Sciences  
 University of California, Berkeley  
 855 California Ave., Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Plate: 603001. row: P. column: 05.  
 Location/Qualifiers  
 /organism="Zea mays"  
 /cvs="B3"  
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 Wang/Bohnert lab"  
 /db\_xref="taxid:31413"  
 /db\_xref="GeneID:1413"  
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 /method="stressed root cDNA library from Wang/Bohnert lab"  
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 Best Local Similarity: 79.18%  
 Query Match: 0  
 Indels: 0  
 Gaps: 0

us-09-720-384a-4 (1-343) x A1637166 (1-602)  
 Oy 183 AAcysAlaLeuSerArgGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 202  
 Db 601 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642  
 Oy 203 LeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 222  
 Db 541 GACACTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 482  
 Oy 223 SerLeuArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 242  
 Db 481 ACATCTGCAAGTGGGAGGTACCGAATCTTCTGCGACCTGCTGCTGCTGCTG 422







